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GenCore version 5.1.6
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OM nucleic - nu	OM nucleic - nucleic search, using sw model	
Run on:	June 15, 2003, 18:20:48; Search time 1282 Seconds (without alignments) 9874.977 Million cell updates/sec	
Title: Perfect score:	US-09-884-987-1_COPY_765_1199	
Sequence:	l aagagaaaggaagtacagaaatgaaatccaaagcttggtc 435	
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched:	2054640 segs, 14551402878 residues	
Total number of	Total number of hits satisfying chosen parameters: 4109280	
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:*

GenEmbl:*

1: 9b_ba:*

2: 9b_htg:*

4: 9b_om:*

5: 9b_om:*

6: 9b_pat:*

7: 9b_pt:*

10: 9b_pt:*

10: 9b_pt:*

11: 9b_sts:*

12: 9b_sts:*

13: 9b_un:*

14: 9b_vi:*

15: 9b_vi:*

16: 9m_fun:*

17: 9m_hum:*

18: 9m_un:*

19: 9m_om:*

20: 9m_om:*

21: 9m_om:*

22: 9m_om:*

23: 9m_om:*

24: 9m_ph:*

27: em_un:*
29: em_un:*
29: em_v1:*
30: em_htg_lum:*
31: em_htg_lum:*
32: em_htg_lum:*
34: em_htg_lum:*
35: em_htg_lam:*
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Pred. No. is the number of results predictedaby chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ACCESSION	247	995							
VERSION	247 FAS	247995.1 FAS GANA	GI:72858	980					
SOURCE	Homo	sapiens	ens.						
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	PRI 15-DEC-1997			ė				Euteleostomi;	; Ношо.				stitute, C.N.R.,	
	linear							Vertebrata;	.; Hominidae				Biology In:	
	p mRNA							Craniata;	Catarrhini				i G., Cell	
	dq 869	RNA.						Chordata;	Primates;				95) Rubert	
	HSFASCDS3	H.sapiens FAS Del3 mRNA	247995	247995.1 GI:728580	FAS gene.	Homo sapiens.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 698)	Ruberti, G.	Direct Submission	Submitted (24-JAN-1995) Ruberti G., Cell Biology Institute, C.N.R.,	
HSFASCDS3	LOCUS	DEFINITION H	ACCESSION 2		KEYWORDS F	SOURCE	ORGANISM H	623	×	REFERENCE 1	AUTHORS R	TITLE D	JOURNAL S	

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ETQNLEGLHHDGQFCHKPCPPDVNMESSRNAHSPATPSAKRKDPDLTWGGFVFFFCQF
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Catarrhini; Hominidae; Homo.
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exons 3 and 4. Exons 5 and 6 translated in a different
frame up to new stop codon at 310."
                                                                                                                                                                                                                                                                                                                                                                                                                On Mar 25, 1995 this sequence version replaced g1:695540.
Location/Qualifiers
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/cell_type="PHA-activated PBMC"
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/db_xref="G1:695541"
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/organism="Homo sapiens"
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/chromosome="10"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 761)
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FAS gene.
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/standard_name="FAS/Apo 1"
/note="Alternative splicing variant of FAS gene missing
exons 3,4 and 6. Exon 5 translated in a different frame up
to a new stop codon at the beginning of exon 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence-experimental
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/protein_id="CAA88033.1"
/db_xref="SPTREMBL:014295"
/translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
ETQNLEGLHHDGQFCHKPCPPDVNMESSRNAHSPATPSAKRK"
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                                                    and Ruberti, G.
The human apoptosis-inducing Fas
1ve splicing
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/note="Translated in a different frame in this variant.
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Immunology, viale C.Marx 43, Rome, Italy, I-00137 2 (bases 1 to 698)

Cascino.1. Flucci.6., Papoff, G. and Ruberti, G. Three functional soluble forms of the human apopto molecule are produced by alternative splicing 95.181785
7533181
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/note="Not translated in this variant."
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/note="Not translated in this variant.
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/standard_name="FAS/Apo 1"
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/db_xref="taxon:9606"
/chromosome="10"
/clone="FAS DEL3"
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nsras46DL
H.sapiens FAS/Apo 1 mRNA for FAS soluble protein (clone FAS
Exc4,6De1).
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ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-APR-1996) Ruberti G., Cell Biology Institute, C.N.R.,
Immunology, viale C.Marx 43, Rome, Italy, I-00137
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335. 396
/note="Translated in a different frame in this variant."
                                                                                                                                    Homo sapiens.

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 836)

Papoff, G., Cascino, I., Eramo, A., Starace, G., Lynch, D. H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Alternative splicing variant of FAS gene missing exons 4 and 6. Exon 5 translated in a different frame up to a new stop codon at the beginning of exon 7."
                                                                                                                                                                                                                                             Ruberti,G.
A N-terminal domain shared by Fas soluble variants prevents cell
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/note="Not translated in this variant as there is
codon at 397."
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/cell_type="PHA-activated PBMC"
1. .399
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/product--FAS Soluble protein-
/protein_id-"CAA94431_1"
/db_xref="G1:1418816"
                                                                                                 270520.1 GI:1418815
FAS soluble protein; FAS/Apo 1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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505. .>836
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/db_xref="taxon:9606"
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J: Immunol. (1996)
2 (bases 1 (to 856)
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/number=1
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/number=2
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                                                                                                                                                                                                                            /standard_name="FAS/Apo 1"
/note="Translated in a different frame in this variant up
to a new stop codon at 310."
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                                                                                                                                      /standard_name="FAS/Apo 1"
/note="Translated in a different frame in this variant."
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/note="Not translated in this variant."
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/note="Not translated in this variant."
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illarity 100.0%; Pred. No. 9.8e-89;
Conservative 0; Mismatches 0;
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    11. .196
    /standard_name="FAS/Apo 1"

/standard_name="FAS/Apo 1"
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                                                                                      'number=2
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X83491
X83491.1 GI:971455
FAS gene.
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                                                                                               GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
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Differential expression of human Fas mRNA species upon peripheral blood mononuclear cell activation
Blochem. J. 310 (Pt 3), 957-963 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-DEC-1994) J. Cheng, University of Alabama at Birmingham, Division of Clinical Immunol. & Rheum., UAB Station, LHRB 473, Birmingham AL 35294-0007, USA (bases 1 to 857)
                                                1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
                                                            AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
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  Length 836,
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100.0%; Score 435; DB 9;
100.0%; Pred. No. 9.7e-89;
11ve 0; Mismatches 0;
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1. 857
/organism="Homo sapiens"
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             Best Local Similarity 100. Matches 435; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Papoff, G., Cascino, I., Eramo, A., Starace, G., Lynch, D.H. and
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                               Length 857;
/isolate="healthy individual"
/db_xref="texon:9606"
/chromosome="10"
/map="10924.1 or 10923"
/clone="pCR TM 11.Fas delta(3,4,6)"
/cell_type="peripheral blood mononucle
391. .762
                                                                                                                                                                                                                                              100.0%; Score 435; DB 9;
llarity 100.0%; Pred. No. 9.7e-89;
Conservative 0; Mismatches 0;
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270519.1 GI:1418817
FAS soluble protein; FAS/Apo 1 gene.
Homo sapiens.
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H.sapiens FAS/Apo 1 mRNA for FAS
Exo4Del).
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                                                                                                                                                                                                        6
                                                                                              /gene="Fas/Apo-1"
391. .637
                                                                                                                                           /note="3 and 4"
700. 762
/gene="Fas/Apo-1"
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                                                                                                                 391. .637
/gene="Fas/Apo-1"
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Best Local Similarity
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REFERENCE
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582 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA 641
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RCRLCDEGHDVNMESSRNAHSPATPSAKRKDPDLTWGGFVFFFCQFH"
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                                                                                                                                                                                                                                                                                                                             'translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
                   Immunology, viale C.Marx 43, Rome, Italy, I-00137
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      this variant up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
                                                                                                                                                                                                 /note="Alternative splicing variant of FAS gene missing exon 4. Exons 5 and 6 translated in a different frame up to a new stop codon at 448."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Translated in a different frame in this variant."
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/number=9
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                                                                                                                                              cell_type="PHA-activated PBMC"
                                                                                                                                                                                                                                                        /evidence=experimental
/product="FRS soluble protein"
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Ruberti, G.
Direct Submission
Submitted (01-APR-1996) Ruberti G.,
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                                                                                     organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397. .459
/note="Translated in a
to a new stop codon at
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543. .567
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                                                                                                               /db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                           'clone-"FAS Exo4Del"
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/number=2
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Matches 435; Conservative
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a soluble form of the Fas
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 920)
Cheng,J., Zhou,T., Liu,C., Shapiro,J.P., Brauer,M.J., Kiefer,M.C., Barr,P.J. and Mountz,J.D.
                                                                                               300
                                                                                                                       301 TATGACACATTGATTAAAGGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 360
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                                                                                                                                                                                                                                                                                                                      Cheng. J.

Cheng. J.

Cheng. J.

Cheng. J.

Direct Submission

Submitted (14-DEC-1994) J. Cheng, University of Alabama at

Birmingham, Division of Clinical Immunol. & Rheum., UAB Station,

LHRB 473, Birmingham AL 35294-0007, USA

J. (bases 1 to 920)

Liu,C., Cheng. J. and Mountz, J.D.

Differential expression of human Fas mRNA species upon peripheral

Blochem J. 310 (Pt 3), 957-961 (1995)
                                                                                               HSFAS34 920 bp mRNA linear PRI 28-
H.sapiens mRNA for Fas/Apo-1 (clone pCRTM11-Fasdelta(3,4)).
X83490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/isolate="healthy individual"
/isolate="healthy individual"
/isolate="healthy individual"
/db_xref="taxon:9606"
/rhomosome="10q24.1 or 10q23"
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/clone="pCR TM 11-Fas delta(3,4)"
/clone="Fas/Apo-1"
/gene="Fas/Apo-1"
/gene="Fas/Apo-1"
/note="and 4"
/note="and 4"
2 a 180 c 186 g 242 t
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/translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
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SNTKCKEEVKRKEVOKTCRKHRKENGGSHESPTLNPETVAINLSDVDLSKYITTIAGV
MTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKD
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100.0%; Pred. No. 9.6e-89;
ive 0; Mismatches 0;
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                                                                                                                                                                           /standard_name="FAS/Apo 1"
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506. .588
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Matches 435, Conservative
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Immunology, viale C.Marx 43, Rome, Italy, I-00137
2 (bases 1 to 945)
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                                                                               408
                                                                                                         GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
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Catarrhini; Hominidae; Homo.
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/note="Alternative splicing variant of FAS gene missing
exon 6"
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Length 920;
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Score 435; DB 9;
Pred. No. 9.6e-89;
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Eukaryota; Metazoa; Chordata;
Mammalla: Eutheria; Primates;
1 (bases 1 to 945)
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100.0%;
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PRI 28-NOV-1995
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                                                      361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA 420
 871 TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 930
                                                                                                                                                                                                                                                                                                                                                                                                                 Cheng,J., Zhou,T., Liu,C., Shapiro,J.P., Brauer,M.J., Kiefer,M.C.,
Barr,P.J. and Mountz,J.D.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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3 (bases 1 to 1104)
Liu,C., Cheng,J. and Mountz,J.D.
Differential expression of human ras with species upon periphera blood monouclear cell activation
Biochem. J. 310 (Pt 3), 957-993 (1995)
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/clone="pCR TM.11-Fas delta TM"
/cell_type="peripheral blood mononuclear cells"
700. 762
/gene="Fas/Apo-1"
                                                                                                                                                                                                                                 SFAS6 1104 bp mRNÀ linear PRI sapiens mRNA for Fas/Apo-1 (clone pCRTM11-FasdeltaTM).
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/db_xref="taxon:9606"
/chromosome="10"
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/gene="Fas/Apo-1"
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Cheng, J.
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808 TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 867
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Key Location/Qualifiers
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strandedness: Double;
topology: Linear;
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/organism-"Homo sapiens"
/db_xref-"taxon:9606"
205 c 217 g 243
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                                                                                                      421 ATCCAAAGCTTGGTC 435
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29-JUL-1997;
CAGACTATCATCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA
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Barr, P.J., Shapiro, J.P. and
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Patent: US 5652210-A 18 29-J
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                                      AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
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AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA 180
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                   AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
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/db_xref="taxon:32644"
309 c 340 g 367
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                                      1 (bases I to 2534)
Screaton, G.R. and Xu, X.
MATERIALS AND METHODS RELATING JO, THE PROTECTION OF
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                                                                                           Patent: WO 9835692-A 4 20-AUG-1998;
SCREATON GAVIN ROBERT (GB); ISIS LAMOVATION (GB)
Location/Qualifiels
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1 (bases 1 to 2534)

1 (Magdara.S., Itch, N. and Yonehara.S. DNA coding for human cell surface an Patent: US 62709998-A 1 07-AUG-2001;
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1 (bases 1 to 2471)

Barr, P.J., Shapiro, J.P. and Kiefer M. Recombinant production of a soluble and thor-1 antigen, fas TM Patent: US 5663070-A 18 62-SEP-1997

Location/Qualifiers
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Sequence 18 from patent US 5663070.
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I63530.1 GI:2481103
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Sequence 4 from Patent W09835692.
A87646
A87646.1 GI:6736281
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                                                   1122 ATCCAAGCTTGGTC 1136
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GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCG

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CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA

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                                                AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
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Nakamura,N. and Nagata,S.
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AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA 180

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence #9 used t	Human Fas soluble	Human cDNA differe	Human Fas soluble	Human Fas antigen	Apoptobody3sc fusi	Fas-delta-TM cDNA.	Soluble Fas recept	Human cell surface
SUMMARIES	ID	ABN79685	AAT34529	ABK84693	AAT34527	AAT34526	AAA39167	AAQ93879	AAX24878	AAQ29959
	DB	24	17	24	17	17	21	16	20	13
	Query Match Length DB	836	920	920	1104	1167	1457	2471	2471	2534
æ	Query Match	100.0	100.0	100:0	100.0	100.0	100.0	100.0	100.0	100.0
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32	٠,	0.00	2551	21	AAC61798	ing a	
35	٦,	0.00	2551	77	ABN/9588	ת	•
	٠,	00.00	8282	21	AAZ34938	CIZSCFAS SULVIVAL	
22	7	0.00	8787	77	AAF 3094 /	CIZSCEAS SULVIVAL	
32	_	0.00	8345	21	AAZ34939		
435	_	0.00	8345	22	AAF30948	Ahhhh survival con	
33.4		9.66	857	17	AAT34530	Human Fas soluble	
33.4		9.66	1468	22	AAA91129	CD44HextraFAStm/cy	
33.4		9.66	1483	22	AAA91130	CD44Hextra/tmFAScy	
33,4		9.66	3009	22	AAA91131	Flt-lextraFAStm/cy	
7		9.66	3009	22	AAA91132	Flk-lextraFAStm/cy	
94.4		90.7	398	24	ABL79512	Human ovarian canc	
83.6		88.2	460	24	ABL80178	Human ovarian canc	
354	_	81.4	975	17	AAT34528	Human Fas soluble	
54		81.4	975	24	ABL63728	Breast cancer rela	
54		81.4	975	74	ABL68887	Kidney cancer rela	
30		75.9	1840	24	ABN79684	Sequence #8 used t	
9.19		38.5	984	14	AAQ48008	Murine Fas gene.	
9.19		38.5	1480	21	AAC61859	DNA encoding a mur	
9		38.5	1480	24	ABN79649	Mouse Fas locus MU	
9.19		38.5	1506	16	AAQ95302	Murine Fas antigen	
9.79		38.5	1506	17	AAT16305	sed	
9.79		38.5	1506	20	AAV71961	Fas ligand (Fast)	
83.4		19.2	338	24	ABN79682	9	
09		13.8	9	24	ABN40425	Human spliced tran	
		13.8	9	24	ABN58759	Human spliced tran	
		13.8	9	24	ABN58760	Human spliced tran	
		13.8	9	24	ABN58963	Human spliced tran	
		6.6	1956	18	AAT67161	Plasmodium falcipa	
1.6		9.6	12177	24	ABL32650	Human immune syste	
8		9.1	744	24	ABL32276	Human immune syste	
		0.1	882	24	ABN70783	ococcus pol	
					ALIGNMENTS		
RESULT 1							
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AAT34529 standard; cDNA; 920
                                     AAT34529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAAACTTCAGAAATGAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand or Fas associated protein-1 is useful for inhibiting expression of Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating hepetitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGAACAĠAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antinfianmatory, hepatotropic, or transmissupplessive, antinfianmatory, hepatotropic. Antisense oligonuclectides were designed to target human Fas. Oligonuclectides were synthesised as chimeric oligonuclectides and are useful for treating an animal having an autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition associated with apoptosis, allograft rejection, or ischemia reperfusion injury. Optionally, the above mentioned conditions are prevented by contacting the allograft with the antisense oligonuclectides. The oligonuclectides are used in diagnostics, therapeutics, prophylaxis and as research reagents and in kits. The oligonuclectides are also useful for research purposes. The present nucleotide sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                     Fas ligand, or Fas associated protein-1 (Fap-1). The inhibition Fas mediated signalling is thought to be immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 435; DB 24; Length 836; 100.0%; Pred. No. 1.8e-108; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                         This invention relates to an antisense compound encoding Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 836 BP; 297 A; 166 C; 183 G; 190 T; 0 other;
                                                               Zhang H;
                                                                                                                                                                                                           Example 18; Page 67-68; 84pp; English.
                                                            Wyatt J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 435; Conservative
                                                            EG,
(MARC/) MARCUSSON E (WYAT/) WYATT J.
                                                                                        WPI; 20Ø2;204886/26.
                                                            Marcusson
                               (ZHAN/) ZHANG H.
                                                                                                        P-PSDB; LABP35574
                                                                                                                                                                                                                                                                                                                                                                                                                                                       related to
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                                                           Dean NM,
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GAATCTCCAACCTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 Human Fas cDNA variants (AA734527-30) are derived from alternative splicing of Fas gene transcripts. They were identified following PCR amplification of CDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angloimmunoblastic lymphadenopathy (AILD) patients and from healthy subjects. In comparison to the Fas gene (AA734526), variant Fas delation (AA734529) has a deletion of nucleotides 391-637. This deletion causes frame shifting and an altered amino acid sequence (AAR99683).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                      angloimmunoblastic lymphadenopathy; ALLD; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natural, soluble form of Fas antigen secreted by human cells is result of alternative mRNA processing – used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 920 BP; 312 A; 180 C; 186 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 435; DB 17;
1larity 100.0%; Pred. No. 1.9e-108;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 121-122; 152pp; English.
                                                Human Fas soluble antigen Fas del3 cDNA.
                                                                                                                                                                                                         Location/Qualifiers
26..307
26..73
7*tag= a
26..73
/*tag= b
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mountz JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US17083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0371263.
10-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOUND
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es 435; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR99684
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                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                WO9620206-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UABR-) UAB
                                                                                                                                                                                                                                                                                  sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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RESULT 2 AAT34529

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA detecting the level of expression of gene(s) (GS) identified by the expression level in an unactivated comparing the expression level in an unactivated (GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of GA least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where
                                                                                                 GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCG 648
                                                                                                                                                        361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA 420
                                                                                                                                                                           TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatold arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcertive colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA differentially expressed in granulocytic cells #1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 1264; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Veissman SM,
                                                                                                                                                                                                                                                                                                                                                                        ABK84693 standard; cDNA; 920 BP
                                                                                                                                                                                                                                    421 ATCCAAAGCTŢGGTC 435
                                                                                                                                                                                                                                                                          ATCCAAAGCTTGGTC 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-435328/46
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                                                                                                                                                                                                                                                                                                                                                                                                             ABK84693;
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the level of expression of the gene is indicative of inflammation;

(4) treating (M5) an inflammation (especially chronic) or in a tissue,
an allergic response in a subject, exposure of a subject to a pathogen
or sterile inflammatory disease, by contacting a tissue having
inflammation with an agent that modulates the expression of gene(s)
from G5 in the tissue. M1 is useful for detecting G6. W2 is useful for
modulating GA, M3 is useful for screening an agent capable of modulating
GCA preferably in an inflammation in a tissue; M4 is useful for
GCA preferably in an inflammation in a tissue; M4 is useful for
inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
c response in a subject, exposure of a subject to a pathogen or sterile
inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
c longeriulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
c eperfusion injury, ARDS, adult respiratory distress syndrome,
inflammatory bowel disease, Crohn's disease, ulcerative colitis,
periodontal disease; also bacterial infection, viral infection,
c parasitic infection, protozoal infection, ingal infection and M5 is
useful for treating one of the above conditions. The present
sequence represents a gene differentially expressed in granulocytes.
C Note: The sequence data for this patent did not form part
c formed directly from WIPO at the control of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 920 BP; 312 A; 180 C; 186 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 435; DB 24;
Pred. No. 1.9e-108;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 100.
Matches 435; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
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100.0%; Pred. No. 2e-108;
11ve 0; Mismatches (
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26..1033
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                                                                                    ATCCAAAGCTTGGTC 435
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26..73
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P-PSDB; AAR99681.
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Best Local Similarity
Matches 435; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
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angioimmunoblastic lymphadenopathy; AILD; ss
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                                                                 Location/Qualifiers
26..970
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74..967
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P-PSDB; AAR99682.
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es 435; Conserv
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                                  Homo sapiens
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transfected to a cell to express the fused gene and then an idiotype antibody is reacted with the expressed cell. The method is useful in medical, pharmacoulatical, pharmacological and biochemical fields. The present sequence encodes a fusion protein designated apoptobody3sc, which is used in the exemplification of the present invention.
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                                                                                                      240
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                                                                                                                                                            Apoptobody3sc fusion protein encoding nucleotide sequence SEQ ID NO:7.
                                                                              AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
                                                                                                               GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
                                                        AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA
                         GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
                                                                                                    AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; fus
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medical; pharmaceutical; pharmacological; biochemical;
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(HAGI/) HAGIWARA H
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Synthetic.
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                                                                                                                                                 1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
                                                                                                Gaps
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                                              Length 1457;
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                                                                                                Indels
Sequence 1457'BP, 441 A, 309 C, 340 G, 367 T, 0 other;
                                         Query Match 100.0%; Score 435; DB 21; Best Local Similarity 100.0%; Pred. No. 2.2e-108; Matches 435; Conservative 0; Mismatches 0;
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1951.1139
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243..1136
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702 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This present sequence is a DNA clone encoding soluble Fas receptor (see AAW98070). The invention provides a method for inhibiting a proinflammatory response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Fas ligand (Fast). In some embodiments, Fast is coadministered with the immunosuppressive agent, and the cell mixture comprises neutrophil cells. The method can be practised in vitro, ex vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neutrophil cells. The method can be practised in vitro, ex vivo in vivo. Suitable immunosuppressive agents include antisense molecules that inhibit endogenous Fasl expression, soluble Fas receptors, ribozymes that inhibit the endogenous expression of Fasl, drugs that inhibit Fasl signalling, agents that inhibit each endogenous expression of endogenous expression of transforming growth factor (TGF)-beta, and polynucleotides coding for an immunosuppressive agent such as TGF-beta. The method can be used for treating diseases associated with an undesired Fasl-mediated proinflammatory response, e.g. graft versus host disease, or an autoimmune disease such as
 rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       systemic lupus erythematosus, rheumatoid arthritis and psoriasis. The invention also provides a method for identifying agents which modulate Fasi stimulation of a proinflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibition of proinflammatory responses - using an agent which modulates FasL stimulation, used for treating graft versus host
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/transl_except= (pos:519..521, aa:Gly)
195..242
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Pred. No. 2.6e-108;
; Mismatches 0;
                                                                           Location/Qualifiers
195..1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4B; 71pp; English.
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Best Local Similarity . 100.0%; Pr
Matches 435; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease or autoimmune disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
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                                                                                                                                                                                                                                      mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psoriasis;
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                                                                                                                                                                                                                                                                                                                                                               Length 2471;
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                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 435; DB 16;
100.0%; Pred. No. 2.6e-108;
tive 0; Mismatches 0;
                                                                                                                                                                                                           claim 3; Fig.3-1 to 3-4; 38pp; English.
                                                                         Shapiro JP;
                                          (LXRB-) LXR BIOTECHNOLOGY INC.
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                                                                         Barr PJ, Kiefer MC,
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                                                                                                                  P-PSDB; AAR76238
              15-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residue is not present in pF3"
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'product= Fas_antigen
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/*tag= e
2518..2523
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P-PSDB; AAR28084.
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A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The CDNA was ligated to BatXI-cut vector pCEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-7 cells which were then suspended in buffer containing murine anti-FRS Ab. The cells were "panned" on plates pre-coated with goat anti-mouse antibodies. The FRS-expressing cells adhered to the plates. Extrachromosomal DNA was prepared from adhered cells and used to transform E.coli VMIOO cells. A 520bp XhOI-BamHI fragment from a positive clone (pFS) was used to screen the KT3 cDNA library. The longest cDNA clone was designated pFSB and contains an ORF corresp.
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                                                                                                                                                                                                                                                                                                                                                                 Length 2534;
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                                                                                                                                                                                                                                                                                                                  Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                 Score 435; DB 13;
Pred. No. 2.6e-108;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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195..1202
/*tag= a
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100.0%;
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                                                                                                                                                                                                                                                                         (i.e. human Fas antigen).
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nes 435; Conŝerv
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SLE;

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Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
                                     hFas doding sequence from plasmid pCEV4/hFas.
                                                                                                                       .ocation/Qualifiers
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/product= E
195..242
/*tag= b
243..1998
              (first entry)
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P-PSDB; AAR92528.
                                                             Fas; antigen;
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06-JUL-1994;
              06-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                              1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                              Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                     AAQ95297 is the plasmid pFS8 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                  Score 435; DB 16;
Pred. No. 2.6e-108;
Mismatches 0;
                                                                                                                                                                                                                                                Example 1; Pages 15-17; 51pp; Japanese
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100.0%;
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            /*tag- b
243..1199
                                    /*tag= c
                                                                                                                                                      (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 435; Conservative
195..242
                                                                                                                                                                            WPI; 1995-202847/27.
P-PSDB; AAR78606.
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                                                                                                                                                                                                                                                                                                                      related diseases
                                                          JP07115988-A
                                                                                                         26-OCT-1993;
                                                                                                                               26-OCT-1993;
 s1g_peptide
                       mat_peptide
                                                                                39-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                       Immunoassay method for soluble Fas antigen in body fluids - for liagnosis of auto:immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 435; DB 17; Best Local Similarity 100.0%; Pred. No. 2.6e-108; Matches 435; Conservative 0; Mismatches 0;
                                                                                                  (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD. (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 49-52; 124pp; Japanese.
                                                                                                                                                                                                               Yonehara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        systemic lupus erythematosus
95JP-0025637
94JP-0154706
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SXB

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prophylactic; AIDS; ss.
                                                                                            Similarity
                                   virus-infected cells.
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                                                                                  AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
                       TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
                                                                                                                     CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAAACTTCAGAAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fas antigen derivative containing modified extracellular region - has low antigenicity, promotes apoptosis and is useful in treatment of viral and other diseases
                                                                                                                                                                                                                                                                                                                                                    apoptosis regulation; gene therapy; lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29 residues are deleted). The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, or by the use
                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                       to mRNA; 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product- Fas_antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
195..1202
                                                                                                                                                                                                                                                                                                                                                    Human; Fas antigen; derivative;
treatment; diabetes; arthritis;
                                                                                                                                                                                          1185 ATCCAAAGCTTGGTC 1199
                                                                                                                                                                    ATCCAAAGCTTGGTC 435
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                                                                                                                                                                                                                                                                                                                                                                            apoptosis modulation; ss.
                                                                                                                                                                                                                                                    AAV07002 standard; cDNA
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                                                                                                                                                                                                                                                                                                                            Human Fas antigen cDNA
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P-PSDB; AAW50289.
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                                                                                                                                                                                                   GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAAATTTATCTGATGTTGACTTGAGT
                                                                                                                                                                                                                                                                  825 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
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CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; l
simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of
                                                                                                                                                   ö
                                                                                                                    Length
                                                                                                                                                   Indels
                                                                                  Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
                                                                                                                 100.0%; Score 435; DB 18;
100.0%; Pred. No. 2.6e-108;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis of lymphocytes can be triggered by the interaction of the cell surface receptor Fas and its ligand Fas. By interfering with this interaction, the method described and its preparations can prevent apoptosis of CD8+ TK lymphocytes caused by expression of Fasi, on activated CD4+ cells. Such Fasi-expressing activated CD4+ cells are especially the result of CD4+ cell infection with an immunodeficiency virus e.g. human immunodeficency virus (SIV). The claimed prevention of apoptosis may then allow annihemence/Feapenstation of cytocoxic T lymphocyte (CT1) activity towards the CD4+ cells infected with the infectious agent, enabling treatment (prophylactic and/or therapeutic) of immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               method of the invention. The method is concerned with reducing depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK) cells in an immune cell population which also comprises of Fas-ligand (Fast)-expressing activated CD4+ cells. It involves contacting this immune cell population with an effective amount of an agent (e.g. a soluble Fas-Fc fusion protein) which would interfere with the interaction between Fas and Fast. Therefore, the method is useful for identifying suitable agents which can reduce depletion of activated Fas-expressing CD8+ TK cells in immune cell populations. Also claimed is the use of the agent in the manufacture of therapeutic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                       кедисіng CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a Fas cDNA sequence used in the method of the invention. The method is concerned with reducing
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1larity 100.0%; Pred. No. 2.6e-108;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  Reducing CD8+ lymphocyte apoptosis to
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 10; 71pp; English.
                                                                                                                           97GB-0003276.
                                                                         98WO-GB00485
                                                                                                                                                                             (ISIS-) ISIS INNOVATION LTD
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P-PSDB; AAW49104.
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435; Conserva
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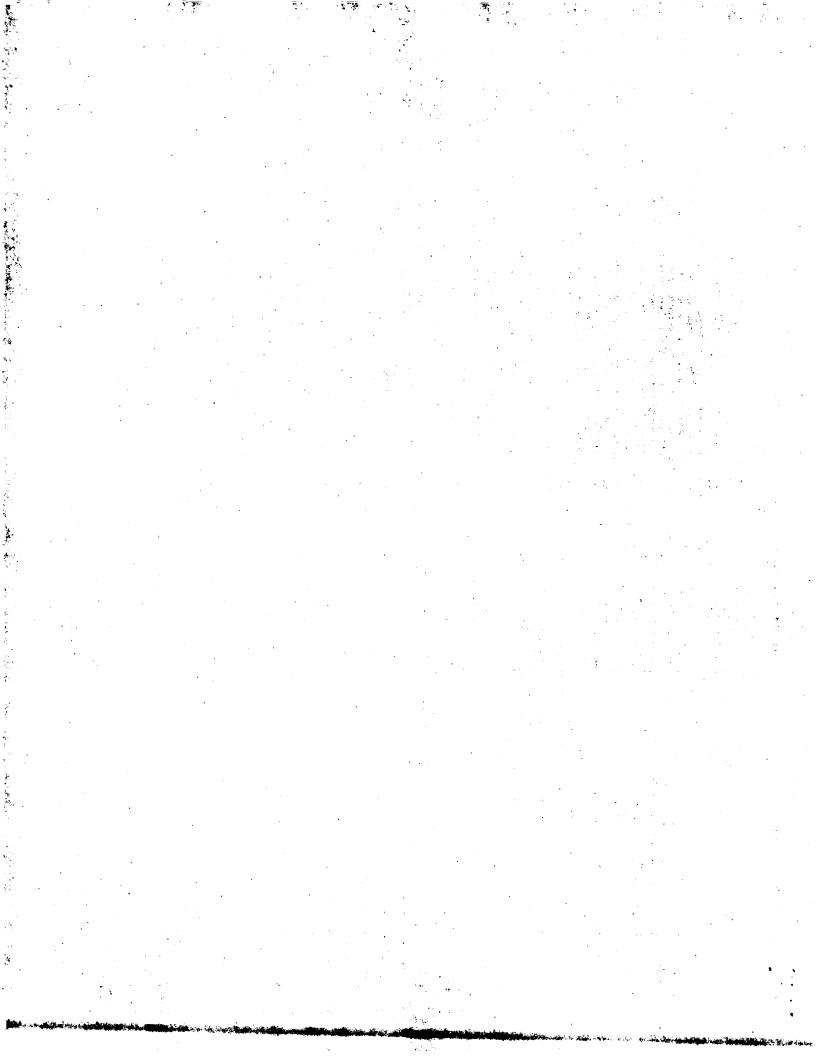
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361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAAACTTCAGAAATGAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
Fas associated protein 1; protein tyrosine phosphatase; cancer;
autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           can also be used to treat cancer, especially colon, liver or lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 71-73; 116pp; English.
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221..1228
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/product= "Fas"
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                                                                                                                          421 ATCCAAAGCTTGGTC
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Page 25-27; 84pp; English.

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This invention relates to an antisense compound encoding
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                                                              AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACÁCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand or Fas associated protein-1 is useful for inhibiting expression of Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating hepatitis
                                                                                                                                     GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
              851 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
                                                                                                                            301 TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
                               AAATATATCACCACTATTGCTGGAGTCATGACCTAAGTCAAGTTAAAGGCTTTGTTCGA
                                                                                                                                                                                                                                                                                                                          tostatic; vasotropic; hepatitis; cancer; allograft rejection;
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18-SEP-2000; 2000US-0665615.
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Fast ligand, or Fast associated protein-1 (Fap-1). The inhibition of Fast mediated signalling is thought to be immunosuppressive, antiinflammatory, hepatotropic, cytostatic and vasofropic. Antisense oligonucleotides were designed to target human Fast oligonucleotides were synthesised as chimeric oligonucleotides and an animal having an autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition associated with apoptosis, allograft rejection, or ischemia reperfusion injury. Optionally, the above mentioned conditions are prevented by contacting the allograft with the antisense oligonucleotide. The oligonucleotides are used in diagnostics, therapeutics, prophylaxis and as research reagents and in kits. The oligonucleotides are also useful for research purposes. The present nucleotide sequence is
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Best Local Similarity 100.
Matches 435; Conservative
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US-09-235-218-2
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US-09-265-315-18
US-09-265-315-18
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US-09-146-249A-35
US-08-206-188B-35
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Pred. No. 3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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100.0%;
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nucleic acid
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/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
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                    Compugen Ltd
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-09-134-001C-1019
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PCT-US95-17083-7
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US-08-444-231-18
US-08-152-443A-18
US-08-152-443A-18
US-08-199-231-18
US-09-180-100-16
US-09-290-640-1
PCT-US95-17083-5
US-09-290-640-65
US-08-259-896B-1
US-08-259-896B-1
US-08-630-822A-61
US-08-630-822A-61
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US-08-630-823A-61
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US-08-630-823A-61
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compu
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Pred. No. 3.2e-109;
Mismatches 0;
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PRIOR APPLICATION UNMBER: USSN 08/371,263
PILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                          TITLE OF INVENTION: SECRETED HUMAN FY
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: COT/US95/17083
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                    Sequence 7, Application PC/TUS9517083 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9517083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 435; Conservative 0;
                                                                   ATCCAAAGCTTGGTC 435
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                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
PCT-US95-17083-7
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TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 360
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3.4e-109;
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                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
APPLICATION NUMBER: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     100.0%; Score 435;
100.0%; Pred. No. 3
Live 0; Mismatché
                                                        JMBER: PCT/US95/17083
CONCURRENTLY HEREWITH
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FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TITLE OF INVENTION: SECR
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 435; Conserv
                                                                                              CLASSIFICATION:
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                                                                           FILING DATE:
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PCT-US95-17083-3
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AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
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Patent No. 5653070
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                              Score 435; DB 1; 1
Pred. No. 4.4e-109;
Mismatches 0;
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755 Page Mill Road
                                                                                                                                                                                                                                                                              100.0%; Sc
100.0%; Pr
tive 0;
            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1122 ATCCAAAGCTTGGTC 1136
                             (415) 813-5600
(415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 ATCCAAAGCTTGGTC 435
                                          TELEFAX: (415) 494-0792
PELEX: 706141
INFORMATION FOR SEQ. ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                              Conservative
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243
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
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195..1136
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Best Local Similarity
Matches 435; Conserv
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FEATURE:
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FEATURE:
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US-08-444-231-18
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APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPINO, JOHN P.
APPLICANT: SHAPINO, JOHN P.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
VUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STARET: California
                                          Length 1167;
                                                                       Indels
                                         100.0%; Score 435; DB 5; I
100.0%; Pred. No. 3.4e-109;
iive 0; Mismatches 0;
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APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444/2:
FILING DATE: 18 MAY-1995
CLASSIFICATION: 530
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REGISTRATION NUMBER: 33,
                                         Query Match 100.
Best Local Similarity 100.
Matches 435; Conservative
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; TOPOLOGY:
PCT-US95-17083-1
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Length 2471; Indels

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LOCATION:
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                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version/#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 435; DB 1; I
Best Local Similarity 100.0%; Pred. No. 4.4e-109;
Matches 435; Conservative 0; Mismatches 0;
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-2006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
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                 Floppy disk
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243
READABLE FORM:
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LOCATION: 195..1136
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; LOCATION:
US-08-152-443A-18
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Application US/08219237B

US-08-219-237B-1

RESULT 7

Sequence 1, Patent No. 5

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APPLICANT: ITOH, Naoto APPLICANT: YONEHARA, Shin TITLE OF INVENTION: DNA COding for Human Cell Surface Antigen
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to an established consensus
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                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-FOS/MS-DOS
SOFTWARE: PATENTIN F2Lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,2378
                                                                                                                                                                                                                                                                                                                                                                     омыЕR: US/08/219,237B
28-MAR-1994
                                                                                                                     ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
                                                                                                                                                                                                            CODNIAL.

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
""""FR: IBM PC COMpatible
"""" PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
RESISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 510
Shigekazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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195..242
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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243..1199
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: double
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LOCATION: 2352..2357
IDENTIFICATION METHOD:
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CLONE: clone pF58
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                                                           1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT 60
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                                 Gaps
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   Length 2534;
                              Indels
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APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STRRET: P.O. BOX 747
CITY: FALLS CHURCH
100.0%; Score 435; DB 2; I
100.0%; Pred. No. 4.5e-109;
tive 0; Mismatches 0;
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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6270998
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NAME: MURPHY JR., GERLAD M.
REGIETRATION NUMBER: 28,977
REFRENCE/COCKET NUMBER: 20-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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MEDIUM TYPE: Floppy disk
 Query Match 100.
Best Local Similarity 100.
Matches 435; Conservative
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ZIP: 22040-0747
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Patent No. 627099
GENERAL INFORMET
APPLICANT. NA
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181 AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
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APPLICANT: NAKAPARA, Shigekazu
APPLICANT: HTGARA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
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                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
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100.08;
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              2534 base pairs
SEQUENCE CHARACTERISTICS:
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195..242
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2352..2357
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2518..2532
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195..1202
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LOCATION:
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Matches 435;
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                                                                                                                 Length 2551;
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                                                                                                                     Score 435; DB 4; I
Pred. No. 4.5e-109;
0; Mismatches 0;
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100.0%; Pred. No. 3.1e-87;
11ve 0; Mismatches 0;
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                                  DATE: 1992-05-25
DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 5:
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CONCURRENTLY HEREWITH
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. Sequence 5, Application PC/TUS9517083
; GENERAL INFORMATION:
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LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 435; Conservative
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APPLICATION NUMBER: PC
FILING DATE: CONCURREN
CLASSIFICATION:
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Matches 354; Conservative
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NUMBER OF SEQUENCES:
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                  10709-10715
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PCT-US95-17083-5.
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
TILLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
SOFTWARE: Patentin Vor: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA
                                                                                                                                                                                                                                                                                              1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                            Length 2534;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                          ; Score 435; DB 4; I; Pred. No. 4.5e-109; 0; Mismatches 0;
          CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09290640 Patent No. 6204055 GENERAL INFORMATION:
                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 435; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 ATCCAAAGCTTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOHNNAL: J. Biol. Chem.
VOLUME: 267
FILE REFERENCE: 1110-207P
                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-180-100-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 2551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-290-640-1
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                                                                                                                                                         TYPE: DNA
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61 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
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                                                                863 IGCIGGIACCAAICICAIGGGAAGAGIGAIGCAIAICAAGAITIAAICAAGGGICICAAA 922
                                        AAAGCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATCATCTTAAGGACATTACT 387
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                                                                                                                                                                 983 AAATCAACCCCAGACACTGGAAATGAAAATGAAGGACAATGTCTGG 1028
                                                                                                                          388 AGTGACTCAGAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 11.6%; Score 50.4; DB 1; Length 7 Best Local Similarity 4.2%; Pred. No. 0.00015; Matches 15; Conservative 200; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
WIWMER OF SEQUENCES: 52
CORRESPONDENCE - ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/935,313 FILING DATE:
                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCHEIFLINGER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 7218 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
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APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
CURRENT FILE REFERENCE: ISPH-0351
CURRENT PRICATION NUMBER: US/09/290,640
NUMBER OF SEQ ID NOS: 85
SOFWWARE: Patentin Ver. 2.0
SEQ ID NO 65
                                                                                                                                                                                                                                                                    GTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACCACTATTGCTGGAGTC 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 ATGACAATCCAGGAAGCTAAAAATTTGCTCGAGAAAATAACATCAAGGAGGGCAAGATA 802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTGGCATCAACTTCATGGAAAGAAGAAGCGTATGACACATTGATTAAAGATCTCAAA 327
                                                                                                     202 AAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAAGTTCAACTG 261
                                                                                                                                                                                      CTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCGTATGACACATTGATTAAAGAT 321
                       GGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCAATGAAGCC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAAGCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACCTTAAATCCTGAAACA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/09290640
Patent No. 6204055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LCCATION: (50)..(1033)
PUBLICATION INFORMATION:
JOURNAL: J. Immunol.
VOLUME: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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181 AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
                                                                                                                 861 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAAACTTCAGAAATGAA 420
388 AATAATATGAATAGTGATCAAGTTGATAAAATACATAGAGAAGAATTAGAAAAAATCGAA 447
                                                                                                                                                    508 GACAAAATGGATCGAGATGCAATTTATAGTATGTATATAGAAGATATAAGTAACAAAAT 567
                                                                                                                                                                                                                                                                                                       628 ATAGATATAAACAAAAAGAAAAAAAAGATATAGATATAGATGTAGACATAGATAAAGAT 687
                                                                                                                                                                                          301 TATGACACATTGATTAAAGATCTCCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATT
                                                                                                                                                                                                                                Gaps
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TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
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Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/08/630,822A
11-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61, Application US/08630822A Patent No. 5840695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLENN R.
, SHIRLEY WU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 261
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2: Floppy disk
IBM PC.compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (303) 863-9700
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ilarity 50.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2706 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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688 ATACATA 694
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Best Local Similarity
Matches 93; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Denver
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MOLECULE TYPE:
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                                                                                                                                                                                                                                1094 RRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAGCTCGACCTGCAGCCAA 1039
                                                                                                                                                                                                          301 TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAA 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/559,896B
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
TITLE OF INVENTION: SEQUESTRIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08559896B
Patent No. 6310046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : USA MRMC - MCMR-JA
FORT DETRICK, FREDERICK
MARYLAND
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Nucleic acid
STRANDEDNESS: Double
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Best Local Similarity
Matches 187; Conserva
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අු	2414	2414 GAACTTAAGGAAGAACTTGAGGAAAAATCTCGTCATATTCAAGAAAGGAAGAAGAAGA 2473	2473
δ	304	304 GACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATTCAG 363	363
qo	2474	2474 GAAAGTTTGGTTCATCAGCTACAATTGCATTAGCTAGAGCTGATTCAGAGGCATTGGCG 2533	2533
Qy	364	364 ACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAAATC 423	423
QQ	2534	2534 AGATCAATAGCTGATGAAAGTATAGCTGATTTAGAAAAGGAAAAGACTATGAAGGAATTA 2593	2593
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Search completed: June 15, 2003, 21:13:05 Job time : 66 secs

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Sequence 6939, Appl
Sequence 70, Appl
Sequence 35, Appl
Sequence 1, Appli
Sequence 8898, Ap
Sequence 8509, Ap
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Watt, Jacqueline
APPLICANT: Watt, Jacqueline
APPLICANT: Shang, Hong
TITLE CO INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: 86/09 602,669
CURRENT FILING DATE: 2001-63-09
PRIOR FILING DATE: 2000-09/19
PRIOR PLING DATE: 2000-09/19
PRIOR APPLICATION NUMBER: US 09/290,640
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Sequence 152, App
Sequence 35, Appl
Sequence 36, Appl
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Sequence 892, App
Sequence 249, App
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Sequence 3002, Ap
Sequence 51, Appl
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0%; Pred. No. 8e-104;
0; Mismatches 0;
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US-08-781-986A-152
US-10-154-251-35
US-10-154-251-36
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US-10-239-67-701-6939
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US-10-084-205-51
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US-09-815-242-8509
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; Sequence 102, Application US/09802669
; Patent No. US20020004490A1
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Best Local Similarity 100.0%;
Matches 435; Conservative 0
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NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 102
LENGTH: 836
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US-09-802-669-102
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Sequence 7, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 11119, A
Sequence 11119, A
Sequence 1156, App
Sequence 198, App
Sequence 111, App
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Sequence 99, Appl
Sequence 1, Appli
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-966-976A-8
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Listing first 45 summaries
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seq length: 2000000000
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Sequence 1, Application US/09884987
Patent No. US20020102653A1
GENERAL INFORMATION:
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(1831)..(1836)
mat_peptide
(243)..()
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LOCATION: (2352)..(2357)
NAME/KEY: polyA_site
LOCATION: (2518)..(2532)
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(195)..(242)
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LENGTH: 2534
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                      AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
                                 825 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
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Pred. No. 1.4e-103;
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APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/949,713
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GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 435; Conservative 0;
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PRIOR APPLICATION NUMBER: US-09
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER-PCT/J
PRIOR FILING DATE: 1997-05-01
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SOFTWARE: Patentin Ver.
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LENGTH: 2534
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                                                                                                                                                                                                           APPLICANT: NAGATA, Shigekazu et al TITLE OE INVERTION: DAM CODING FOR HUMAN CELL SURFACE ANTIGEN FILE REFERENCE: 020-4877 CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: ~2001-06-21
NUMBER OF SEO ID NOS': 11
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100.0%; Pred. No. 1.4e-103;
tive 0; Mismatches 0;
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APPLICANT: Ferrick, David A.
APPLICANT: Swift, Susan E.
APPLICANT: Armstrong, Randall
APPLICANT: Box, Bryan
TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige
TITLE OF INVENTION: Secretion and Switch Rearrangement
FILE REFERENCE: A-66038-4/MS/JJD/DER
CURRENT APPLICATION NUMBER: US 09/076,956,976A
PRIOR APPLICATION NUMBER: US 09/076,624
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; Patent No. US20020133076A1
; GENERAL INFORMATION:
                                                                                                                              . Sequence 7, Application US/09966976A
; Patent No. US20020168649A1
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                   1211 ATCCAAAGCTTGGTC 1225
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
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Best Local Similarity 100.0
Matches 435; Conservative
   421 ATCCAAAGCTTGGTC
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                                                                                                                                                                                                                 DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
                                                                                                                          Sequence 1, Application US/09802669
Patent No. US20020004490Al
                   1185 ATCCAAGCTTGGTC 1199
                                                                                                                                                 Patent NO. COLLEGERERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
ADDI.TCANT: Marcusson, Elic G.
ADDI.TCANT: Marcusson, Elic G.
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
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Matches 435; Conservative
421 ATCCAAAGCTTGGTC
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PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
ISSUE. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES: 10709-10715
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LOCATION: (22)
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Length 8345; Indels

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TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige TITLE OF INVENTION: Secretion and Switch Rearrangement
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                                                                                                                                                                                                       100.0%; Score 435; DB 9; I ilarity 100.0%; Pred. No. 2.6e-103; Conservative 0; Mismatches 0;
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; Patent No. US20020123076A1
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CURRENT FILING DATE: 2001-09-25
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Armstrong, Randall
                                                                                                              ORGANISM: Artificial sequence
                                       ersion 3.1
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   1998'-05-12
                                                                                                                                                  ; OTHER INFORMATION: Synthetic US-09-966-976A-8
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Best Local Similarity
Matches 435; Conserva
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SOFTWARE: Patentin ve
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   PRIOR FILING DATE/
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SEQ ID NO 8
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                                                                          LENGTH: 8345
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                                                                      TITLE OF INVENTION: Methods and compositions for Screening for Modulators and Ige SynTITLE OF INVENTION: Secretion and Switch Rearrangement
FILE REFERENCE: A-66039 37RMS/JP/DLR
CURRENT APPLICATION NUMBER: US/09/963,206B
CURRENT FILING DATE: 12/001-09/25
PRIOR APPLICATION NUMBER: US/09/076,624
PRIOR FILING DATE: 1998-05/12
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TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Syn
TITLE OF INVENTION: Secretion and Switch Bearrancent
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Pred. No. 2.6e-103;
Mismatches 0;
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FILE REFERENCE: A-66038 4/RMS/JD/DLR
CURRENT APPLICATION NUMBER: US/09/966, 976A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 09/076,624
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Best Local Similarity 100.0%;
Matches 435; Conservative 0
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                                      Armstrong, Randall
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Ferrick, David A.
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                    Swift, Susan E
                                                         Fox, Bryan
                                                                                                                                                                                                                                                                                               ORGANISM: Artificial
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS
SOFTWARE: PatentIn ve
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122 GAATCTCCAACCTTAGATCCTGAAACAGGCAATAAATTTATCTGATGTTGACTTGAGT 181
                                                                                                       181 AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
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                                   121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
                                                     CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAAACTTCAGAAATGAA
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Patent No. US2002013237A1
GENERAL INPORMATION:
APPLICANT: Joiles, Paul A.
APPLICANT: Joiles, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
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Pred. No. 2.2e-93;
0; Mismatches 2;
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CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASELSEQ for Windows Version 4.0
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; OTHER INFORMATION: n = A,T,C or
US-09-867-701-2490
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Best Local Similarity 99.5%;
Matches 395; Conservative
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                                                                                      1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
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                  Length 8345;
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                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411.756 CURRENT APPLICATION NUMBER: US/09/918,995 CURRENT FILING DATE: 2001.07-30 PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR APPLICATION NUMBER: US/09/235,076 NUMBER OF SEQ ID NOS: 38054 SOFTWARE: PASLED FOR WINDOWS VERSION 3.0 SEQ ID NO 17119
                Score 435; DB 10;
Pred. No. 2.6e-103;
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llarity 97.9%; Pred. No. 6.7e-96;
Conservative 0; Mismatches 8
                                                   0; Mismatches
                100.0%; Score 435;
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Publication No. US20030073623A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17119
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                                   100.0%;
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                                 al Similarity 100.
435; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Watt, Jacqueline
APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR PLING DATE: 2000-09-18
PRIOR PPLING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
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Pred. No. 1.2e-82;
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100.0%; Pred. No. 1...
0; Mismatches
                  CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT APPLICATION NUMBER: US/06/233,133
PRIOR PLICATION NUMBER: US/60/233,133
PRIOR PLICATION NUMBER: US/60/234,009
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR PLILNG DATE: 2000-09-10
PRIOR PLILNG DATE: 2000-09-20
PRIOR PLILNG DATE: 2000-09-20
PRIOR PLILNG DATE: 2000-09-20
PRIOR PLILNG DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR PLILNG DATE: 2000-09-22
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Patent No. US20020004490A1
GENERAL INFORMATION:
      Gene Sets
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Matches 354; Conservative
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LENGTH: 184
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391
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                                                                  CCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATCCTCAAGGACATTACTAGTG
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APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TILLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastEQ for Mindows Version 4.0
SEQ ID NO 3156
                                                                                                                                                        392 ACTCAGAAATTCAAACTTCAGAAATGAAATCCAAAG 428
                                                                                                                                                                                    361 ACTCGGAAAATTCAANCTTCAGAAATGAAATCCAAAG 397
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Pred. No. 1.6e-90;
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Patent No. US20020165180A1
GENERAL INFORMATION
APPLICANT: Weaver, Zoe
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Best Local Similarity 99.0%;
Matches 386; Conservative
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US-09-867-701-3156
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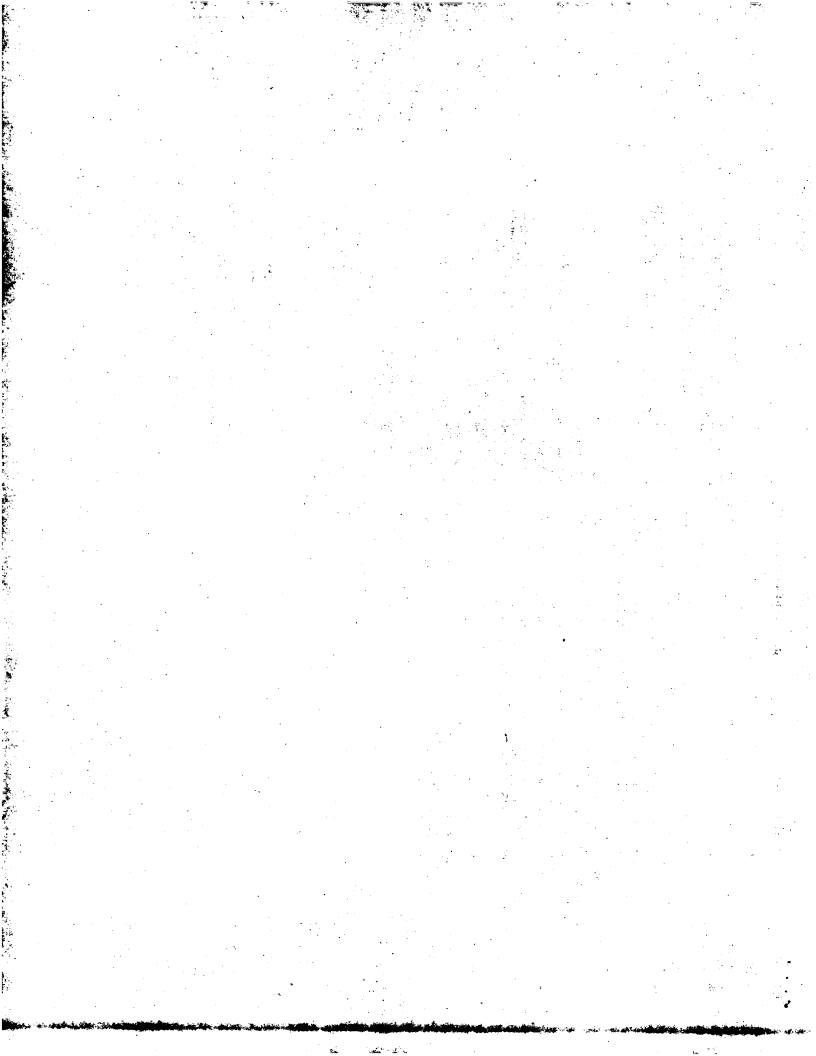
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134 CTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCA 193
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GENERAL INFORMATION:
TATLE OF INVENTION:
TITLE OF INVENTION:
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TOTALE OF INVENTION:
CURRENT PILIGE ACID SEQUENCES OBTAINED
CURRENT PAPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PSESEE FOR WINDOWS VERSION 3.0
SEQ ID NO 15171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 496;
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100.0%; Pred. No. 3.3e-69;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                    US-09-918-995-15171
; Sequence 15171, Application US/09918995
; Publication No. US20030073623A1
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OTHER INFORMATION: n = A,T,C or G
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Matches 302; Conservative
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TC 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCAATGAAGCCAAAATAGATGATGA 217
                                                                                                                                                                                                                                                                                    146 GTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCA 205
                                                                                                                                                                                                                                                                                                                                                                                           AACTTCATGGAAAGAAAGAAGCGTATGACACATTGATTAAAAGATCTCAAAAAAGCCAATC 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 TTTGTACTCTTGCAGAGAAATTCAGACTATCATCATCAAGGACATTACTAGTGACTCAG 397
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                                                                                                        Length 1840;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: uS/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 AAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGGTC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 AAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGGTC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 69.4%; Score 302; DB 9; L
Best Local Similarity 100.0%; Pred. No. 3.3e-69;
Matches 302; Conservative 0; Mismatches 0;
                                                                                                        Score 330; DB 10;
Pred. No. 3.1e-76;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13045
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13045, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LCCATION: (1)...(489)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-13045
                                                                                                        75.9%;
98.5%;
                                                                                                       Query Match 75.9
Best Local Similarity 98.5
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                  ; NAME/KEY: CDS
; LOCATION: (95)...(426)
US-09-802-669-101
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US-09-918-995-13045
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122

242



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June 15, 2003, 19:50:58; Search time 1424 Seconds (without alignments) 4947.357 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                         OM nucleic - nucleic search, using sw model
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US-09-884-987-1_COPY_765_1199 Title: Perfect score:

1 aagagaaaggaagtacagaa...........atgaaatccaaagcttggtc 435 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

16154066 seqs, 8097743376 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

em_estba:* em_esthum: em_estro: em_estmu: em_estpl: em_estov em_htc:* gb_est1

em_estfun: em_estom:* gb_htc:# gb_est3: gb_est4: gb_est5:

em_gss_other:* em_gss_rod:* em_gss_mam:* :unj_esp_ma em_gss_hum:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ø					
Result		Query					
Q	Score	Match	Match Length DB	DB	П		Description
-	433.4	9.66	509	10	AW994695		AW994695 RC1-BN003
7	429.8	98.8		14	BQ051037	•	BO051037 AGENCOURT
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S	394.4	7.06	398	6	AA180032		AA180032 ZO93q12.r
9	383.6	88.2		6	AA293570		AA293570 zt25h11.r

W05802 za89f05.rl AV651157 AV651157	⊣.	Ξ.	AV715411 AV715411	\equiv	H02935 yj46b08.rl	ALS42093 ALS42093		ob18g12.	0 603052	8 EST291	AJ392468 AJ392468	ALS42092 ALS42092	4	AL071063 Drosophil	BJ441951 BJ441951	BJ436174 BJ436174	1 BJ3791	SP_013	ω	5 1M0037	_	BJ36	~:	BJ41	_	BJ389689 BJ389689		4	24059		а 6	BJ391376 BJ391376	BJ328095 BJ328095	BJ414027 BJ414027	BJ361397 BJ361397	BJ410037 BJ410037	
W05802 AV651157	BE070451	AABOUUDB	AV715411	AA852070	H02935	AL542093	AK002590	AA745982	BI766250	. AW141748	AJ392468	AL542092	AL566565	CNS00FUH	BJ441951	BJ436174	BJ379111	AZ175342	AI231531	AZ318375	BJ345089	BJ363187	C90546	BJ413360 .	BJ360248	BJ389689	BJ364065	BJ387004	BJ324059	BJ388447	BJ323809	BJ391376	BJ328095	BJ414027	BJ361397	BJ410037	
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ALIGNMENTS

RESULT 1 AW994695	
rocns	AW994695 509 bp mRNA linear EST 05-JUN-2000
DEFINITION	RC1-BN0039-060200-011-a05 BN0039 Homo sapiens CDNA, mRNA sequence.
ACCESSION	
VERSION	AW994695.1 GI:8254929
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 509)
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.
	Nagai, M.A., da Silva, W. Jr., 2ago, M.A., Bordin, S., Costa, F.F.,
	Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, P.H.,
	Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Háre
	, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
	Simpson, A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF &xpressed
	sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3494 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.
	Laboratory of Cancer Genetics
	Ludwig Institute for Cancer Research
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
	Brazii
	Tel: +55-11-2704922 Fax: +55-11-2707001

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BI254532 62978522F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123477 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
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                                                                                                                                                                                                                                                                                                                                                    /clone_lib-"NIH_MGC_71"
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/lab host-"BH10B (phage-resistant)
/note-"Organ: uterus; Vector: pCMV-SPOR76; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT-Average insert size 2.1 kb.
1 221 c 215 g 267 t
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 NIH-MGC.http://mgc.nci.nih.gov/.
National Instituees of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12873 row: } column: 23
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Pred. No. 3.9e-90;
0; Mismatches 2; Indels
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/clone="IMAGE:5785846"
                                                       rausberg, Ph.D.
                                                                                                                                                                                                                                         High quality sequence stop: 689
Location/Qualifiers
                                                       Contact: Robert Strausberg, F
Email: cgapbs-rømail.nih.gov
Tissue Prochement: ATCC
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Best Local Similarity 99.5%;
Matches 431; Conservative
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BI254532
BI254532.1 GI:
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
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VERSION
KEYWORDS
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                 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-RC1-BN0039-060 200-011-a05&t3-200-02-06&t4=1) 269 primer: puc. 18 forward High quality sequence stop: 509.
Location/Qualifiers
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Site_l: Smal; A minl-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
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5', mRNA sequence.
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1055)
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                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%; Score 433.4; DB 10; Length 509;
llarity 99.8%; Pred. No. 5.1e-91;
Conservative 0; Mismatches 1; Indels 0;
 Email: asimpson@ludwig.org.br
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BQ051037.1 GI:19810377
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NHH MGC http://mgc.nci.nlh.gov/.
National Institutes/of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert grausberg, Ph.D.
Emali: cgapbe:rfmail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life machinologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM1301 row: 1 column: 06
High quality sequence stop: 757.
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                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InbeE:5123477"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH108"
                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc.
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Pred, No. 5.3e-86;
0; Mismatches 0;
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llarity 99.5%;
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RESULT 4 BF126149

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BF126149 809 bp mRNA linear EST 24-OCT-2000 601650407F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:3934273 5',
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                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgabbe remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM774 row: n column: 02
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                                                                                                                                                   1 (bases 1 to 809)
NIH-WGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e-84;
0; Mismatches 1;
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Location/Qualifiers
                                                             BF126149.1 GI:10965189
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99.3%;
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Best Local Similarity 99.35
Matches 429; Conservative
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                                  mRNA sequence.
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1 (bases 1 to 460)
1 (billier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags 97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                     AA293570 460 bp mRNA linear EST 08-AUG-1997 2L25hll.rl Soares ovary tumor NbHOT Homo sapiens CDNA clone IMAGE:714213 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GGCATCAACATCAAGGAAAGAAAGAAGCGTATGACACATTAAAGATCTCAAAAAAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1853 Std Error: 0.00
Seq primer: -28ml3 rev2 Er from Amersham
High quality sequence stop: 125.
Location/Qualifiers
                                                                                                AGATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAAGTTCAACTGCTTCGTAATT
                                                                                                                                                                                                                     CCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATCCTCAAGGACATTACTAGTG
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                                                                            MO 63108
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/clone_lib-"Soares ovary tumor NbHOT"
/sex-"Female"
                                                                                                                                                                                                                                                                                                                      ACTCAGAAAATTCAAACTTCAGAAATGAAATCCAAAG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:5934710"
/db_xref="taxon:9606"
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , mRNA sequence.
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1 (bases i to 398)

1 (bases i to 398)

Chissoe, S. Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M.; Hullman, M., Kucaba, T., Ledy, M., Le, M., Le, N., Mardis, E., Moore, Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Thierry-Meg, J., Trevaskis, E., Generation and analysis of 280#000 human expressed sequence tags
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                                                                                                                                                                                                                     EST 31-DEC-1996
                                                                                                                                                                                                               AA180032 398 bp mRNA linear EST 31-DEC-1996 zo93g12.rl Stratagene ovarian cancer (#937219) Homo sapiens CDNA clone IMAGE:594502 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR
                    61 CAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACCACTATTGCTGGAGTCATGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 CAATAAATTTATCTGATGTTGACTTGAGTAAATATTATCACCACTATTGCTGGAGTCATGA 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28HN3 rev2 from Amersham High quality sequence stop: 263.
361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 6.1e-82;
0; Mismatches 2;
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/db_xref="taxon:9606"
/clone="IMAGE:594502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                               (HUMAN);, mRNA sequence.
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AA180032.1 GI:1761298
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al Similarity 99.5%;
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Chinese National Human Genome Center at Shanghai
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W05802 GI:1278534
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                      Score 383.6; DB 9; Pred. No. 2.1e-79;
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/clone-"IMAGE:299745"
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Best Local Similarity 99.0%;
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Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J.; Liu,F., Huang,O., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/lab_host="DH10B (ampicillin resistant)"
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xhor"
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 2012013, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzgeforg.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                         /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
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20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCCMD03"
/clone_lib="GLC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        74 C.
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Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-BT0407-020
300-122-d09&t3=2000-03-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 50
High quality sequence stop: 395.
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//dev_stage="Adult"
//note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2:
//note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2:
//note="Organ: breast; Vector and by products derived
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//16 - Ludwig Institute for Cancer Research) profiles
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HGBBT125 Human Glialblastoma Cell Homo sapiens CDNA, MRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Hd
1 (bases 1 to 305)
Jin, H. L., Hu, S.N., Tu, C., Yuan, J.G. and Olang, B.Q.
DDRT-PCR of Humen Filalblastoma Cell Line BT-325 CDNAs
Unpublished (1997)
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llarity 95.5%; Pred. No. 2e-5
Conservative 0; Mismatches
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/clone_lib="BT0407"
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E 1 (bases 1 to 1152)

S NIH-MGC http://morgincl.nih.gov/.

National Instructes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert/Strausberg, Ph.D.

Email: cgapbert/Strausberg, Ph.D.

Email: cgapbert/Strausberg, Ph.D.

Contact: Robert/Strausberg, Ph.D.

Email: cgapbert/Strausberg, Ph.D.

Contact: Robert/Strausberg, Ph.D.

Contact: Robert/Strausb
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5', mRNA sequence.
BM922638
BM922638.1'GI:19373017
EST.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host=*E.coli DH5a*
//note=*Organ: Brain: Vector: PCRII, Invitrogen; Total RNA
was isolated from human glialblastoma cell line BT325.
Then Differential Display RT-PCR was conducted between
normal and all-trans Retinoic Acid induced cell.
Bifferentially expressed PCR products were cloned and
sequenced. "
Contact: Bogin Qiang
National Laboratory of Medical Molecular Biology, CAMS & PUMC
Institute of Basic Medical Sciences, Peking Union Medical College &
Chinese Academy of Medical Sciences
5 Dong Dan San Tiao. Beijing 100005, P.R. China
Tel: (010)65296411
Fax: 8610-524629
Email: zh357&iname.com
Seq primer: Mi3 Reverse Primer.
Location/Qualifiers
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100.0%; Pred. No. 1.1e-56;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                           1. .305
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human Glialblastoma Cell"
/cell_type="Glialblastoma Cell"
/cell_line="BT-325"
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Matches 286; Conservative
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
COMMENT
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BM922638
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AV715411 DCB Homo sapiens cDNA clone DCBAUC01 5', mRNA sequence.
AV715411 GI:10796928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 GCAGAAACAGAAAGTTCCACTGCTTTCCAATTGGGCATCAACTTCATGGGAAAGGAAAG 769
                                                                                                                                                                                                                                                                                                                                        //note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIMGC Library."
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 696)
Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCGTATGACACATT-GATTAAAGATCTCAAAAAA---GCCAATCTTTGTACTCTTGCA
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12795 row. c column: 21
High quality sequence start: 52
High quality sequence stop: 628.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1152;
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Pred. No. 1.6e~51;
0; Mismatches 23
                                                                                                                                                                                                                                              /clone="IMAGE:575724"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH108"
                                                                                                                                                                                                   /organism="Homo sapiens'
                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.7%;
Best Local Similarity 91.3%;
Matches 337; Conservative (
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'db_xref="taxon:9606
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National Laboratory of Medical Molecular Biology, CAMS & PUMC
Institute of Basic Medical sciences, Peking Union Medical College &
Chinese Academy of Medical Sciences
5 Dong Dan San Tiao, Beijing 100005, P.R. China
Tel: (010)65296411
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HGBBT116 Human Glialblastoma Cell Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA 180
Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
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Jin, H.L., Hu, S. N., Tu, C., Yuan, J.G. and Qiang, B.Q.
DDRT-PCR of Human Glialblastoma Cell Line BT-325 cDNAs
,G., Cheng, Z. and Han, Z.
Homo sapiens CDNA DCB clones
Unpublished (2000)
Contact: Seguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoy/In Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P.R. China
Tel: 86/21-50801929
Fax: 86/21-50801922
Emajá: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
141 c 156 g 189 t
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0
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                  Emaj4: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.3%; Score 201.2; DB.10
Best Local Similarity 98.5%; Pred. No. 7.3e-37;
Matches 203; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                      /clone_lib="DCB"
/cell_type="dendritic cells"
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DCBAUC01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .217
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: M13 Reverse Primer
                                                                                                                                                                                                                                                                                                                  /dev_stage="mature"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: zh357@iname.com
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AA852070
LOCUS
DEFINITION
ACCESSION
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KEYWORDS
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ORGANISM
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COMMENT
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EST 20-JUN-1995
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57 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 461)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The Washu-Warck EST Project
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                         /note="Organ: Brain; Vector: PCRII, Invitrogen; Total RNA was isolated from human glialblastoma cell line BT325.
Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell.
Differentially expressed PCR products were cloned and seminanced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1432 Std Brror: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                     Score 196.4; DB 9; Length 217;
Pred. No. 8.2e-36;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
/clone_lib="Human Glialblastoma Cell"
/cell_type="Glialblastoma Cell"
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/db_xref="GDB:563902"
                                                       /cell_line="BT-325"
/lab_host="E.coli DH5a"
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Location/Qualifiers
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Insert Size: 1432
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Best Local Similarity 99.5%;
Matches 197; Conservative
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IMAGE:151767
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                                                        AL542093 932 bp mRNA linear EST 16-FEB-2001 AL542093 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE009Y106 5 prime mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                    264 TCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCGTATGACACATTGATTAAAGATCT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                  324 CAAAAAAGCCAATCTTTGTACTCTTGCAGAAAATTCAGACTATCATCCTCAAGGACAT 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 932)
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BP 191 91006 EVRX cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                        Length 461;
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                          /clone_lib="Soares placenta Nb2HP"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flangulitech.com URL :
http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                     Score 172; DB 14;
Pred. No. 4.4e-30;
                                                                                                                                                                                                                                                                           39.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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/lab_host-"DH108"
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/db_xref-"taxon:9606"
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/clone="CS0DE009Y106"
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Matches 172; Conservative
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                                        Gaps
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  Length 932;
                                        Indels
  DB 9;
Score 169.4; DB
Pred. No. 2e-29;
1; Mismatches
38.9%;
98.3%;
Query Match 38.9
Best Local Similarity 98.3
Matches 170; Conservative
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Search completed: June 15, 2003, 21:11:49 Job time : 1428 secs

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(without alignments)
2749.125 Million cell updates/sec
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750
1 GWLCLLLDPIPLIVWVKRKE......KANLCTLAEKIQTIILKDIT 145
                                                                                                                                  June 15, 2003, 21:13:09; Search time 1535 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4109280
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                        OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2054640 seqs, 14551402878 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                            BLOSUM62
Xgapop 10.0, Xgapext (Ygapop 10.0, Ygapext Fyagop 6.0, Fgapext Delop 6.0, Delext
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Maximum DB seq length: 200000000
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PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_lt:*
4: gb_om:*
5: gb_ow:*
6: gb_pt:*
7: gb_pt:*
10: gb_pt:*
11: gb_sts:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	7994 H.sapi	0519 H.sapiens	A83490 H.Sapiens m F05336 DNA encodin	5160	87646 Sequence	3572 Sequenc	3438 Seq	10 CDNA	21 CDNA	4 Hu	3111	17 H.sapiens		100	1540	2	536 Sequenc	Ξ.	238	995 H.	520 H	191 H.sapiens	993 H	193 H. sapie	equence 1	0 Macaca f	Macaca n	8	Cercoce	Macaca		AA331230 Sequence	Saniene	44835	32357 Macaca a	342 H.sapiens	5384 csnptnfrs	286 н.	57394 Human DN	021299 Oryctola	AB021296 Oryctolag
SUMMARIES	ID	SCD	S4DE	HSFAS34	E35160	8764	AR163572	~	E05110	E09121	HUMFASANT	AR143111	HSAPOI	BC0124/9	- ا		AX060542	AX060536	HSFASAPOA	AX060538	HSFASCDS3	9		HSFASCDS1	HSFAS6	158632	AB031420	4485	AF326208	AF344843	AF344833	AY00/5/2	AA331330	777	4483	33	APT9	. G75384	6	573	2129	AB021296
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	Result No.													,	ပ	נ'																	÷									

ALIGNMENTS

RESULT 1

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899 bp mRNA linear PRI 30-JUN-1996 for FAS soluble protein (clone FAS
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Direct Submission
Submitted (01-APR-1996) Ruberti G., Cell Biology Institute, C.N.R.,
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Catarrhini; Hominidae; Homo.
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                                          /note="Not translated in this variant. /number=9
                                                                                                                                           761
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Matches:
Conservative:
Mismatches:
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Z70519.1 GI:1418817
FAS soluble protein; FAS/Apo 1 gene.
                430. .>761
/standard_name="FAS/Apo 1"
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                                                                      /evidence-experimental
  /evidence=experimental
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Mammalia; Eutheria; Primates;
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H.sapiens FAS/Apo 1 mRNA
Exo4Del).
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J. Immunol. (1996)
2 (bases 1 to 899)
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Best Local Similarity:
                                                                                     261
                                                                                                                               Alignment Scores:
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HSFAS4DEL
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              PRI 15-DEC-1997
                                                                                                                                              /evidence-experimental
/product-FAS soluble protein"
/protein_id="CAM8803_1"
/db_xref="G1:695541"
/tbanslation="MIGIWILDFULFVARESSKSVNAQVTDINSKGLELRKTVTTV
/translation="MIGIWILDFULFVARESSKSVNAQVTDINSKGLELRKTVTTV
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/note="Translated in a different frame in this variant up
to a new stop codon at 310."
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 761)
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/note="Translated in a different frame in this variant."
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                                                                                                                                                                                                                                                                                                             On Mar 25, 1995 this sequence version replaced gi:695540.
Location/Qualifiers
1. .761
                linear
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/standard_name="FAS/Apo 1"
/note="Not translated in this variant."
/number=8
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/note="Not translated in this variant.
           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                      cell_type="PHA-activated PBMC" .312
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'standard_name="FAS/Apo 1"
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/standard_name="FAS/Apo 1"
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/number=1
                                                                                                                                                                                                                                                                                                                                              1. ./or
/organism="Homo sapiens"
              761 bp
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                                                                                                                                                                                                                                                                                                                                                                   /isolate="GF"
/db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                             /clone="FAS DEL2"
                      H.sapiens FAS Del 2 mRNA.
247994
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                                                      247994.1 GI:728579
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                                                                               Homo sapiens.
              HSFASCDS2
                                                                     FAS gene.
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DEFINITION
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SFAS34 920 bp mRNA linear PRI 28-NOV-1995 sapiens mRNA for Fas/Apo-1 (clone pCRTM11-Fasdelta(3,4)).
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                                                                                                                                                ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
                                                                                                                                                                                                                                                 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
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Cheng,J., Zhou,T., Liu,C., Shapiro,J.P., Brauer,M.J., Kiefer,M.C.,
Barr,P.J. and Mountz,J.D.
                                                                     AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                           Liu,C., Cheng,J. and Mountz,J.D.
Differential expression of human Fas mRNA species upon peripheral blood mononuclear cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Station,
                                                                                                                                                                                                        /isolate="healthy individual"
/db_xref="taxon:9606"
/chromosome="l00"
/map="l0q24.1 or 10q23"
/clone="pcR TM 11-Fas delta(3,4)"
/cell_type="peripheral blood mononuclear cells"
//consorted consorted consorted consorted cells"
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96013198
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Location/Qualifiers
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/gene="Fas/Apo-1"
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180 c 18
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ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
RCRLCDEGHDVNMESSRNAHSPATPSAKRKDPDLTWGGFVFFFCQFH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135. .396
'note="Translated in a different frame in this variant.
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Immunology, viale C.Marx 43, Rome, Italy, I-00137
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197. .459
/note="Translated in a different
co a new stop codon at 448."
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                 /cell_type="PHA-activated PBMC"
1. .450
/standard_name="FAS/Apo 1"
                                                                                                                                                                                                                       /evidence-experimental
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/db_xref="GI:1418918"
/db_xref="SPTREMBL:014292"
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'note="Not translated in
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/note="Not translated in
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/note="Not translated in
                                            organism="Homo sapiens"
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                                                                      /db_xref="taxon:9606"
/chromosome="10"
                                                                                                    clone-"FAS Exo4Del"
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                                                        /isolate="LN"
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750.00
100.00%
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/number-2
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/number=1
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/number=3
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Query Match:
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101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
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C12115/09,AGIK31/00,AGIK48/00,C07K16/42,C07K19/00,C12N5/10, PC
C12N15/02//
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Matches:
Conservative:
Mismatches:
Indels:
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Hagiwara H., Actsuka,Y. and Miyahara,J.
Method for inducing apoptosis
Patent: JP 2000102389-A 7 11-APR-2000;
YOSHIHIDE HAGIWARA,HIDEAKI HAGIWARA
OS Artifical Sequence
PN JP 2000102389-A/7
PD 11-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                           243
             1. .1008
/organism="Homo sapiens"
/db_xref="taxon:9606"
205 c 217 g 24
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    Location/Qualifiers
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JP 2000102389-A/7.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1008)
                                                                                                                                                                                                     ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                               920
145
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    .1008
/product='Fas protein'

                                                                                                  US-09-884-987-2_COPY_175_319 (1-145) x HSFAS34 (1-920)
                                                   Conservative:
Mismatches:
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Patent: JP 1993219959-A 2 31-AUG-1993;
OSAKA BIO SCI KENKYUSHO
                               Length:
Matches:
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strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1008 bp
DNA encoding human Fas protein.
E05336
E05336 I GI:2173525
JP 1993219959-A/2.
Homo sapiens.
Filter
                                                                       Indels:
                                                                                 Gaps:
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OSRDA JUICHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      topology: Linear;
*source: cell_line=KT-3;
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JP 1993219959-A/2
                          3.64e-71
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                                                 Percent Similarity:
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PAT 31-JAN-2002

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ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
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ARI63572
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Nagata,S., Itoh,N. and Yonehara,S.
DNA coding for human ced1 surface
Patent: US 6270998-A 1 N2-AUG-2001
                                                                                         Gaps:
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487 c 503 q
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                                                                                                                                                                                                      unidentified
unclassified.
1 (bases 1 to 2534)
Screaton, G. R. and Xu. X.
MATERIALS AND METHODS RELATING/TO THE PROTECTION OF USEFUL IMMUNE
                                                                                                                                                                                                                                            ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
                                                                                                                                                                                                                                                                                   LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
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                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                 Location/Qualifiers (7) (1317).
Location/Qualifiers
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SCREATON GAVIN ROBERT (GB);/ISIS IN
Location/Qualifiers
1. .2534.
/Organism="unidentified"
/db_xref="taxon:32644"
                                              1. 1457
/organism="unidentified"
/db_xref="taxon:32644"
1 309 c 340 g 36
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Sequence 4 from Patent W09835692.
A87646.1 GI:6736281
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C12R1:91)
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DB:
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PAT 17-OCT-2001

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

A87646

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1077 ATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAAATTCAGACTATCATC 1136
                                                                                                                                                                                                                                                                                                                                             PAT 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostom1;
897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTC
                                                                                              AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys
                                                                                                                                                                                                          IleLysaspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle
                                         ThrilealaGlyValMetThrLeuSerGlnValLySGlyPheValArgLySAsnGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSADA JUICHI, ITO NAOTO, YONEHARA SHIN
CIZNI5/12,CIZNI5/85//CIZP21/00,(CIZNI5/12,CIZRI:91),
                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; E
Catarrhini; Hominidae;
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1831. .1836
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195. .242
243. .1199
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*source: cell_line*KT-3;
*source: clone=pFSB;
Feature is identified by simil.
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| Location/Qualifiers | 1. .2534 | /Organism="Homo sapiens" | /db_stref="taxon:9606" |
| 817 a | 487 c | 503 g | 727
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27-JUL-1993
27-APR-1992 JP 1992107323
26-APR-1991 JP 91P 125234
                                                                                                                                                                                                                                                                                                                                             E05110 2534 bp
CDNA encoding human Fas antigen.
E05110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primates;
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PC (C12P21/00,C12R1:91);
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                                                                                                                                                                                                                                                                             1137 CTCAAGGACATTACT 1151:
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hypothetical: No;
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JP 1993184368-A/1.
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Mammalia; Eutheria;
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mat_peptide
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Homo sapiens
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                                                      717 GGGTGGCTTTGTCTTTTTTGCCAATTCCACTAATTGTTTGGGTGAAGAAAGGAA 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777 GTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACC 836
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                            1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu 20
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                                                                                 21 ValGinLysThrCysArgLysHtsArgLysGluAsnGlnGlySerHtsGluSerProThr
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  US-09-884-987-2_COPY_175_319 (1-145) x AR163572 (1-2534)
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Conservative:
Mismatches:
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Nakamura, N. and Nagata, S.
Fas antigen derivatives
Patent: US 6306395-A 16 23-OCT-2001;
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Sequence 16 from patent US 6306395.
AR173438
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487 c 503 g
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i (bases 1 to 2534):
Itoh, N., Yonehara, S., Ishii, A., Yonehara, M., Mizushima, S., Sameshima, M., Hase, A., Seto, Y. and Nagata, S.
The polypeptide encoded by the CDNA for human cell surface antigen
                                                                                                                                                                                                                                                                                                                                               AsnGluAlaLyslleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fas antigen; cell surface antigen; transmembrane protein.
Homo sapiens (clone pF58) (tissue library: pCEV4) cDNA to mRNA.
Homo sapiens
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Human Fas antigen (fas) mRNA, complete cds.
                                                                                                                                                                                                                                                                     US-09-884-987-2_COPY_175_319 (1-145) x E09121 (1-2534)
/cell_type='cancer c
/cell_line='KT3'
1. 188
189. 1202
/product='hFas'
                                                                                                                                                                                                      Conservative:
Mismatches:
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Matches:
                                                                                                                             727
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/organism="Homo sapiens"
                                                             203. .2534
                                                                                                             /db_xref="taxon:9606"
487 c 503 g
                                                                            Location/Qualifiers
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Cell 66 (2), 233-243 (1991)
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1 (bases 1 to 253)
1 Yonehara, S., Kishi, S., Nishimura, K., Yamazaki, Y. and Kobayashi, Y. PRODOTTION OF SOLUBLE MEMBRANE PROTEIN AND SOLUBLE MEMBRANE PROTEIN PARAPHAT 1995115988-A 2 09-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                    PAT 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                        ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
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                                                                                                                                                                                ValGlaLysThrCysArgLysHisArgLysGluAsnGlaGlySerHisGluSerProThr 40
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PI YONEHARA SHIN, KISHI SHUJI, NISHIMURA KEIKO, YAMAZAKI
YOSHIAKI, PI KOBAYASHI YUKO
PC C12P21/02,C12N1/21,C12N15/02,C12N15/09,C12P21/08,(C12P21/02,
                                                                                                                                GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu
                                                                                                                                                                                                                                  LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
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strandedness: Double;
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              Length:
Matches:
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Indels:
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JP 1995115988-A/2
                                                                                                     US-09-884-987-2_COPY_175_319 (1-145)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         topology: Linear;
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CDNA encoding hFas.
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Homo sapiens
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                              Score:
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PRI 06-MAR-1995

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1077 ATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAAAAATTCAGACTATCATC 1136
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Dean, N.M. and Marcusson, E.G.
Antisense inhibition of Fas mediated signaling
Patent: US 6204055-A 1 20-MAR-2001;
Location/Qualifiers
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H.sapiens mRNA for APO-1 cell surface antigen.
X63717
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Mismatches:
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Sequence 1 from patent US 6204055
AR143111.1 GI:15104397
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493 c 508 g
                                       LeuLysAspIleThr 145
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Query Match:
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AR143111
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TITLE
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SNTKCKEEGSRSNLGWLCLLLLPI PLI VWVKRKEVQKTCRKHRKENQGSHESPTLNPE
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           Location/Qualifiers
1. 2534
/organism="Homo sapiens"
                                             /db_xref="taxon:9606"
/clone="pF58"
                                                                                'tissue_lib="pCEV4"
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                                                                      /cell_line="KT3"
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/gene="fas"
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/gene="fas"
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/gene="fas"
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/gene="fas"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2719)
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garci
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                  863 TTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC
                                                                                                              LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                     ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                                                                                                           AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys
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//Lisue_Lype="Bladder, transitional cell papilloma"
//clone_lib="NIH_MGC_93"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens, Similar to tumor necrosis factor receptor superfamily, member 6, clone MGC:21432 IMAGE:4514272, mRNA, complete cds.
BC012479
BC012479.1 GI:15214691
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/db_xref="taxon:9606"
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Tissue Procurement: ATCC
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LLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL
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                                                                                                                                                                                    Submitted (10-FBB-1992) P.H. Krammer, German Cancer Research Center, Tumorimmunology Program, Im Neuenheimer Feld 280, 6900 Heidelberg. FRG

2 (Dases 1 to 2551)

2 (Dases 1 to 2551)

Chan, A., Behrmann, I., Falk, W., Pawlita, M., Maier, G., Li-Weber, M., Richards, S., Dhein, J., Trauth, B.C., Postlagl, H. and Krammer, P. H. Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor of Ecceptor superfamily. Sequence identity with the Fas antigen J. B.O.I. Chem. 267 (15), 10709-10715 (1992)
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                                                                                   Eukaryoča, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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                        APO-1 gene; cell surface antigen
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ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
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'note="Vector: pCMV-SPORT6"
                       /codon_start=1
/product="Similar to tumor
                                           superfamily, member 6"
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/db_xref="G1:15214692"
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Mismatches:
                                            /organism="synthetic construct"
/db_xxef="taxon:32630"
/note="synthetic"
2249 c 2040 g 2101 t
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Patent: WO 0134806-A 7 17-MAY-2001;
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           Rigel Pharmaceuticals, Inc. (US)
                      Location/Qualifiers
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-Q=CQR01_1/USPPO_spool/USO8084987/runat_09062003_140300_13165/app_query.fasta_1.327
-Q=CQR01_L/USPPO_spool/USO8084987/runat_09062003_140300_13165/app_query.fasta_1.327
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DCALIGN-200 -THE_ESCORE-ptc -THE_MAX-100 -THE_MIN-0 -ALIGN-15.
-USER-USO9884987_eCGN_11_208_erunat_09062003_140300_13165 -NCPU-6 -ICPU-3
-NOAMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPELOCK-100 -LONGLOG
-PBV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                   4 Human Fas cDNA variants (AAT34527-30) are derived from alternative splicing of Fas gene transcripts. They were identified following PCR amplification of cDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angloimmunoblastic lymphadenopathy (ALLD) patients and from healthy subjects. In comparison to the Fas gene (AAT34520), variant Fas del3 (AAT34529) has a deletion of nucleotides 391-637. This deletion causes frame shifting and an altered amino acid sequence (AAR99683).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu
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                                                                                                                                                                               Natural, soluble form of Fas antigen secreted by human cells result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                   Disclosure; Page 121-122; 152pp; English.
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sig_peptide
                  mat_peptide
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chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation:

(4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
661 ATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAAATTCAGACTATCATC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are modulating (MX) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening for an agent capable of modulating GCA or an inflammation (especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to detecting (M1) granulocyte (GC) activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA differentially expressed in granulocytic cells #1264
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                                                                                                                                                                                                                                                                                                                                                                                              ABK84693 standard; cDNA; 920 BP
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glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at few lined-pot_sequences:
                                                                                                                                                                                                                                                                                                                            480
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                                                                                                                                                                                                                                                                                                                                                        ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
                                                                                                                                                                                                                                                                                                         LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fas antigen; autolmmune disease; systemic lupus erythematosus; SLE; angioimmunoblastic lymphadenopathy; AILD; ss.
                                                                                                                   other;
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Mismatches:
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                                                                                                                                                                        Best Local Similarity:
Query Match:
DB:
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                                                                                                                   Sequence 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A cDNA clone (AAT34526) codes for a membrane receptor-like protein, Fas antigen (AAR996B1). It was isolated from cDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angioimmunoblastic lymphadenopathy (AILD) patients, and from healthy subjects, by PCR amplification. In addition to fascoble for PCR products were obtd. (see also AAT4527-30). These coded for soluble forms (AAR996B2-85) of Fas antigen that are present thigher levels in SLE and AILD patients than the non-soluble Fas
                                                                                                                                                                                                                                                                                                                                                                              is
                                                                                                                                                                                                                                                                                                                                                                          Natural, soluble form of Fas antigen secreted by human cells result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
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Matches:
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Best Local Similarity:
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                                                                                                                                                                             22-DEC-1995;
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1012 ACTATTGCTGGAGTCATGACCTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGC 1071
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ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                                                                                                                                          81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ29959 standard; cDNA to mRNA; 2534 BP
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121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrlleIle 140
                   The present invention describes a method for causing apoptosis in which a fused gene consisting of a gene participating to apoptosis and a gene encoding at least the variable region of anti-idiotype antibody is transfected to a call to express the fused gene and then an idiotype antibody is reacted with the expressed cell. The method is useful in medical, pharmacoutical in paramaceutical, pharmacological and blochemical fleids. The present sequence encodes a fusion protein designated apoptobody3sc, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                        Apoptobody3sc fusion protein encoding nucleotide sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                         Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion gene;
medical; pharmaceutical; pharmacological; biochemical; ds.
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Matches:
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Mismatches:
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/product= "apoptobody3sc"
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                                                                                    968 CTCAAGGACATTACT 982
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(HAGI/) HAGIWARA H.
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Synthetic.
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                                                                      A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The CDNA was ligated to BatxI-cut vector pCEV4 via BatxI linkers. The KT3 cDNA library was used to transfect monkey COS-7 cells which were then suspended in buffer containing murine anti-Fas Ab. The cells were panned on plates pre-coated with goat anti-mouse antibodies. The Fas-expressing cells adhered to the plates. Extrachromosomal DNA was prepared from adhered cells and used to transform E.coli VMIO0 cells. A 520bp XhoI-BamHI fragment from a positive clone (PF3) was used to screen the KT-3 cDNA library. The longest cDNA clone was designated pF58 and contains an ORE corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrIleAlaGlyValMetThrLeuSerGlnValLySGlyPheValArgLySAsnGlyVal
DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monoclonal antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                                          other;
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Mismatches:
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Matches:
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                                                   Claim 3; Fig 1 and 2; 27pp; English.
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AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
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                                                                                                                                                                                                                                                          Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                          AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of related diseases.
Plasmid pF58; human Fas cDNA; soluble membrane protein;
           antibody production; diseases; treatment; prevention;
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Matches:
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                                               Location/Qualifiers
195..1202
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16
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243..1199
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                                                                           195. 242
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P-PSDB; AAR78606.
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Best Local Similarity:
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                              Homo sapiens
                                                                                                                            JP07115988-A
                                                                                                                                                                    26-OCT-1993;
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                                                                            sig_peptide
                                                                                                mat_peptide
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contg. human Fas cDNA.

Plasmid pF58

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AAT16303 RESULT 셤

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1017 GTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGAAGCGTATGACACATTG 1076
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                                                                                                                                 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu
                                                                                                                                                                                               21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
                                                                                                                                                                                                                                                                                                                                                                       61 ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                                                                                                                                                                                                                    41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
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                                                                US-09-884-987-2_COPY_175_319 (1-145) x AAT16303 (1-2534)
                      Gaps:
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/product= Fas_antigen
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195..1202
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243..1199
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                    1077 ATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAAAATTCAGACTATCATC 1136
IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the coding sequence for the human Fas antigen contained within the plasmid pCEV4/hEas. The soluble Fas antigen is included in the immunoasay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas monoclonal antibody, as well as the standard soluble Fas antigen encoded by this sequence. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoasay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as
                                                                                                                                                                                                                                                                                                                                                                                             Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE; rheumatoid arthritis; serum; systemic lupus erythematosus; ss:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis or systemic lupus erythematosus (SLE)
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Matches:
Conservative:
Mismatches:
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/product= Fas antigen
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                                                                                                                                                                                                                      ВP
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                                                                                       141 LeuLysAspileThr 145
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94JP-0154706
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P-PSDB; AAR92528.
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Best Local Similarity:
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06-JUL-1994;
                                                                                                                                                                                                                                                                                                        06-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
  121
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Fasl;

(first entry)

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Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL, CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; Simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
                                                                                                                                             prophylactic; AIDS; ss
    18-NOV-1998
                                           as cDNA.
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                                                                                                 Fas antigen derivative containing modified extracellular region -
has low antigenicity, promotes apoptosis and is useful in treatment
of viral and other diseases
                                                                                                                                                                                                               The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferrably at least 29 residues are deleted).

The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                            Disclosure; Fig 1-2; 102pp; Japanese.
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  Nakamura N;
                                                                                                                                                                                                                                                                                                                                                                                                                           virus-infected cells.
                                       WPI; 1997-558981/51
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Best Local Similarity:
                                                          P-PSDB; AAW50289
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Nagata S,
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ID AAV
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The present sequence represents a Fas cDNA sequence used in the method-of the invention. The method is concerned with reducing depletion of activated Fas-expressing CD8+ Tlymphocyte killer (TK) cells in an immune cell population which also comprises of Fas-ligand (FasL)-expressing activated CD4+ cells. It involves contacting this immune cell population with an effective amount of an agent (e.g. a soluble Fas Fc fusion protein) which would interfere with the interaction between Fas and FasL. Therefore, the method is useful for identifying suitable agents which can reduce depletion of activated Fas-expressing CD8+ TK cells in immune cell populations. Also claimed is the use of the agent in the manufacture of therapeutic compositions. Apoptosis of Immune cell populations and its ligand FasL. By interfering with this interaction, the method described and its preparations can prevent apoptosis of CD8+ TK lymphocytes caused by expression of FasL on activated CD4+ cells. Such FasL-expressing activated CD4+ cells. Such man immunodeficiency virus (HTV) or simian immunodeficiency virus e.g., human immunodeficiency virus (HTV) or simian immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  naintenance/regeneration of cytotoxic T lymphocyte (CTL) activity towards the CD4+ cells infected with the infectious agent, enabling treatment (prophylactic and/or therapeutic) of immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
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                                                                AAV32993 (1-2534)
 Mismatches:
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Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
                                                                                                                                           5'-untranslated
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                                                                                                                  The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5'-untranslation, translational start site, translational termination region or 3'-untranslated region of hucleic acid molecules encoding Fas, Fas ligand (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine phosphatase). The antisense compounds are used to inhibit the expression of Fas, FasL or Fapl in cells or tissues. They are used to treat autoimmume or infilammatory diseases such as hepatitis. They can also be used to treat cancer, especially colon, liver or lung
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                                          1 (Fap-1) expression
                                                                                                                                                                                                                                                                                                          cancer or lymphoma
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Best Local Similarity:
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81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
61 ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                       comprises combining a candidate bloactive agent, optionally linked to a fusion partner, with a cell comprising a fusion nucleic acid composed of the IL-4 inducible epsilon promoter (see AAZ34932), and a reporter gene, such as the present death gene. The promoter is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising an inducible epsilon promoter chimeric
Fas-IRES-hygromycin-bovine growth hormone poly-A tail placed
in vector (12s backwards so that no leaky transcription occurs
through the CMV promoter. It is an example of a death gene that
provides a nucleic acid that encodes a protein which causes a
provides a nucleic acid that encodes a protein which causes a
methods of in The death gene can be used as a reporter gene in
methods of the invention used to screen for modulators of IgE
synthesis, secretion and switch rearrangement. The method
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IGE; antibody; modulator; screening; human; allergy; therapy;
reporter; Cl2ScFas; survival construct; ss.
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                                                                                                                                                                                                                                                                                                                                                                                           1163 CTCAAGGACATTACT 1177
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Chimeric - Bos taurus.
Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-062297/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antisense compound targeted to nucleic acid encoding Fas, Fas
ligand or Fas associated protein-1 is useful for inhibiting expression
of Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating
hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to an antisense compound encoding Fas, Fas ingand, or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated signalling is thought to be immunosuppressive, antiinflammatory, hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were designed to target human Fas. Oligonucleotides were synthesised as chimeric oligonucleotides and are useful for treating an animal having an autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition associated with apoptosis, allograft rejection, or ischemia reperfusion injury. Optionally, the above mentioned conditions are prevented by contacting the allograft with the antisense oligonucleotide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotides are used in diagnostics, therapeutics, prophylaxis and as research reagents and in kits. The oligonucleotides are also useful for research purposes. The present nucleotide sequence is
cytostatic; vasotropic; hepatitis; cancer; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
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                                                                                         Location/Qualifiers
221..1228
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18-SEP-2000; 2000US-0665615.
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(MARC/) MARCUSSON E G.
(WYAT/) WYATT J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related to human Fas.
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P-PSDB; ABP35562.
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Query Match:
DB:
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                                                          Homo sapiens
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or absence of the
       Absence of the reporter gene indicates
                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin E; allergy; therapy; switch rearrangement; vector; Fas; survival construct; death gene; ds.
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                        Sequence 8282 BP; 1892 A; 2249 C; 2040 G; 2101 T; 0 other;
                                           8282
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presence
                                                  Matches:
Conservative:
Mismatches:
Indels:
                                            Length:
then induced with IL-4 or IL-13, and the
      reporter gene is detected. Absence of that the agent inhibits the promoter.
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                                                        Percent Similarity:
Best Local Similarity:
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                                     Alignment Scores
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                                                                                                                                            The present sequence is that of survival construct C12ScFas in which the interleukin-4 inducible epsilon promoter-chimeric Fas(CD95)-internal ribosome entry site-hygrowycin-bowine growth hormone polyA tail is placed in the C12s vector backwards so that no leaky transcription occurs through the CMV promoter. Methods of the invention utilise diphtheria toxin for screening purposes, especially for identifying modulators of 1gE synthesis, secretion and switch rearrangement. A claimed method of screening for bloactive agents capable of inhibiting the IL-4 inducible epsilon promoter (see AAF30941), which is involved in 1gE switching, comprises: combining a candidate bloactive agent and a cell that does not endogenously express heparin-binding epidermal growth comprises; combining HBEGF, inducible epsilon promoter and nucleic acid comprising the IL-4 inducible epsilon promoter and colling diphtheria toxin to the cell; and determining whether the cell is dead. Survival constructs carrying a death gene and a dring selectable marker have been used to generate an epsilon concert survival cell line. Inhibitors of 1gE synthesis can be identified that prevent the production of 1gE and reduce or eliminate an allergic response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibiting a promoter, especially promoter involved in immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8282 BP; 1892 A; 2249 C; 2040 G; 2101 T; 0 other;
Screening for agents capable of inhibiting a promoter, interleukin-4 inducible epsilon promoter involved in in production, by using diphtheria toxin constructs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-884-987-2_COPY_175_319 (1-145) x AAF30947 (1-8282)
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121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
                                                               21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr.
                                                                                                                                                                                                                        101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin E; allergy; therapy; switch rearrangement; vector;
Fas; survival construct; death gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-4 inducible epsilon promoter; human; IgE; antibody;
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C comprising an inducible epsilon promoter-chimeric Fas (either CD8

C or mLyL2)-IRES-lydromycin-bovine growth hormone poly-A tail placed

In vector Cl2s backwards so that no leaky transcription occurs

through the CMV promoter. It is an example of a death gene that

C provides a nucleic acid that encodes a protein which causes a

cell to die. The death gene can be used as a reporter gene in

methods of the invention used to screen for modulators of 1gB

C synthesis, secretion and switch rearrangement. The method

comprises combining a candidate bloactive agent, optionally linked

to a fusion partner, with a cell comprising a fusion nucleic acid

composed of the IL-4 inducible epsilon promoter (see AA234932), and

a reporter gene, such as the present death gene. The promoter is

then induced with IL-4 or IL-13, and the presence or absence of the

contract gene is detected. Absence of the reporter gene indicates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods, cell lines and vectors for screening for modulators of immunoglobulin E synthesis, secretion and switch rearrangement
                                                                                                                                                                                                IgB; antibody; modulator; screening; human; allergy; therapy; reporter; survival construct; ss.
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                                                                                                                                                                                  Interleukin-4 inducible epsilon promoter; immunoglobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Armstrong R, Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reporter gene is detected. Absence o that the agent inhibits the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 13A-C; 81pp; English
                                                                             AA234939 standard; DNA; 8345 BP
99WO-US10497.
                                                                                                                                                                                                                                                                                                                                                                   98US-0076624
                                                                                                                                28-FEB-2000 (first entry)
                                                                                                                                                        Ahhhh survival construct.
                                                                                                                                                                                                                                 Chimeric - Homo sapiens.
Chimeric - Bos taurus.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                             (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrick DA, Swift SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-062297/05.
                                                                                                                                                                                                                                                                                      W09958663-A1
                                                                                                                                                                                                                                                                                                                                           12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                .8-NOV-1999
                                                                                                     AAZ34939;
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BP

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The present sequence is that of survival construct Ahhhh in which the interleukin-4 inducible epsilon promoter-chimeric Fas(CD8 or mLyt2)-internal ribosome entry site-hygromycin-bovine growth hormone polyA tail is placed in the Cl2s vector backwards so that no leaky transcription occurs through the CMV promoter. Methods of the invention utilise diptheria toxin for screening purposes, especially for identifying modulators of IgE synthesis, secretion and switch rearrangement. A claimed method of screening for
                                                                                                  Screening for agents capable of inhibiting a promoter, especially interleukin-4 inducible epsilon promoter involved in immunoglobulin production, by using diphtheria toxin constructs -
                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 13A-C; 80pp; English.
WPI; 2001-335931/35.
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US-09-884-987-2_COPY_175_319 (1-145) x AAZ34939 (1-8345)

8345 145 0 0 0

Conservative: Mismatches:

4.68e-82 750.00 100.00% 100.00%

Best Local Similarity: Percent Similarity:

Score:

Query Match:

Indels:

Length: Matches:

99US-0165189.

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bloactive agents capable of inhibiting the IL-4 inducible epsilon promoter (see AAF30941), which is involved in IgE switching, comprises: combining a candidate bloactive agent and a cell that does not endogenously express heparin-binding epidermal growth factor (HBEGF) and which comprises a fusion nucleic acid comprising the IL-4 inducible epsilon promoter and a nucleic acid encoding HBEGF; inducing the promoter with IL-4; adding diphtheria toxin to the cell; and determining whether the cell is dead. Survival constructs carrying a death gene and a promoter survival cell line. Inhibitors of IgE synthesis can be identified that prevent the production of IgE synthesis can be eliminate an allergic response.
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Sequence 8345 BP; 1915 A; 2264 C; 2084 G; 2082 T; 0 other;

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Alignment Pred. No. Score: Percent S: Best Loca. Query Matc	Alignment Sco Pred. No.: Score: Bescent Simil Best Local Si Query Match:	Alignment Scores: Pred. No.: Score: Score: Frecent Similarity: 100.00% Ouery Match: 22	8	Length: Matches: Conservative: Mismatches: Indels:	8345 145 0 0 0	
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ογ	7		urenteurenP	rolleProLeuile	/alTrpValLysArgLysGlu	20
a	4401		TCTTCTTTGC	CAATICCACIAATI	GGGTGGCTTTGTCTTCTTTTGCCAATTCCACTAATTGTTTGGGTGAAGAAAGGAA	4342
ογ	21		SArgLysHisA	rgLysGluAsnGln	ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr	. 04
đ	4341		CAGAAAGCACA	GAAAGGAAAACCAA(GTACAGAAAACATGCAGAAAGGCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACC	4282
ογ	41		rvalAlaileA	snLeuSerAspVall		09
qa	4281		AGTEGCAATAA	ATTTATCTGATGTT	TTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC	4222
ογ	. 61		MetThrLeus	erGlnValLysGly	ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal	80
qq	4221		CATGACACTAA	GTCAAGTTAAAGGCT	ACTATTGCTGGAGTCATGACACTAAGTCAAGGTTAAAGGCTTTGTTCGAAAGAATGGTGTC	4162
ογ	81		eAspGluIleL	ysAsnAspAsnVal		100
q	4161		AGATGAGATCA	AGAATGACAATGTC	AATGAAGCCAAAATTAGATGAGATCAAGAATGACAATGTCCAAGACACAGGAAAA	4102
ογ	101		gAsnTrpHisG	lnLeuHisGlyLys		120
qa	.4101		TAATTGGCATC	AACTTCATGGAAAG	GTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCGTATGACACTTG	4042
οy	121		SLysAlaAsnL	euCysThrLeuAlac		140
qq	4041		AAAAGCCAATC	TTTGTACTCTTGCAC	ATTABAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC	3982
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Search completed: June 15, 2003, 22:07:31 Job time: 226 secs

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US-09-133-944-2

US-09-208-827-2

US-09-21-0178-626

US-09-134-001C-2243

US-08-11-729-9

US-08-11-729-9

US-08-131-462-3

US-08-131-462-1

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US-09-131-001-1

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US-09-131-001C-1838

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US-09-131-001C-1838

US-09-131-001C-1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
            -017B-149
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US-08-098-327E-45
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Indels:
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Matches:
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APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/17083
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application PC/TUS9517083 GENERAL INFORMATION:
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100.00%
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LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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606
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2137
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Best Local Similarity:
Query Match:
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-Q-Cqqn2_1/19206/app_query.fasta_1.327
-Q-Cqqn2_1/192PO_spool/Ros984887/runat_09062003_140301_13206/app_query.fasta_1.327
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-LSGPEXT-0 -UNITS-blts -START-1 -END-1 -WATRIX-blosum62. TRANS-hummad40.cdi
-LSGT-45 -DGCALIGN-300 -THR_SCORES-EDCT -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-USER-USO9884987_@CGN_11_36_@ctunat_09062003_140301_13206 -NCPU-6 -ICPU-3
-NO_MADP -LAGREDUERY NEG_SCORES-0 -WAIT -DSPBLOCK-100 -CONGLOG-
-EDGY_TIMEOUT-120 -WARN_TIMEOUT-30 -THRADS=1 -SGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
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Sequence 1, A
Sequence 16,
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Sequence 18,
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Sequence 5, P
Sequence 65,
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Sequence 1,
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                                                                             ; Search time 64 Seconds
            GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/Pcurg.COMB.seq:*
/cgn2_6/ptodata/2/ina/packfiles1.seq:*
                                                        nucleic search, using frame_plus_p2n model
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/cgn2_6/ptodata/2/1na/5B_COMB.seq:
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US-08-152-443A-18
PCT-US95-17083-5
US-09-290-640-65
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US-09-290-640-1
PCT-US95-17083-9
PCT-US95-17083-3
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PCT-US95-17083-1
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US-08-468-560C-1
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Perfect score:

Title:

Sequence:

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Scoring table:

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ASnGlualaLySIleAspGluIleLySASnAspAsnValGlnAspThrAlaGluGlnLyS 100
                    728 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTC 787
                                                                                           788 AATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAA 847
                                                                                                                                                                907
                                                                                                                                               101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu
   APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: ITOH, Naoto
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by similarity with known sequence to an established consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Virginity: Virginity: Virginity: Arlington STATE: Virginity: Arlington STATE: Virginity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08219237B Patent No. 5874546 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
                                                                                                                                                                                                                                                                           141 LeuLysAspileThr 145
                                                                                                                                                                                                                                                                                                             968 CTCAAGGACATTACT 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to MRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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LOCATION: 195.,1202
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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STRANDEDNESS: double
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CLONE: clone pF58
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LOCATION:
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                                                                                                                                                                  21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
                                   GTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACC
                                                                                                                                              ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                       LeuAsnProGluThrValAlaileAsnLeuSerAspValAspLeuSerLysTyrIleThr
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Mismatches:
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Matches:
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APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED HUMAN FINUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9517083 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 LeuLysAspIleThr 145
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Best Local Similarity:
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PCT-US95-17083-1
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APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                              COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linea
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Best Local Similarity:
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US-08-468-560C-1
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 by similarity with known sequence or
to an established consensus
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. (6270998
GENERAL INFORMATION:
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                                                                                                                  NAME/KEY: polyA_site
LOCATION: 1831..1836
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                           NAME/KEY: mat_peptide
LOCATION: 243.1199
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                                                                                                       NAME/KEY: polyA_site
LOCATION: 2352..2357
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LOCATION: 2518..2523
IDENTIFICATION METHOD:
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ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFERAX: 703-205-8050
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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243..1199
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195..242
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1831..1836
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APPLICANT: NAGATA, Shigekazu APPLICANT: ITOH, Naoto

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Signaling
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                                                                                                                                                                                                                                                    APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                Sequence 1, Application US/09290640 Patent No. 6204055 GENERAL INFORMATION:
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                                                                                                                                       141 LeuLysAspileThr 145
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LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver.
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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DATE: 1992-05-25
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                                837 TTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAGATA, No. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURREWT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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Conservative:
Mismatches:
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Sequence 16, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
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US-09-180-100-16
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Best Local Similarity:
Query Match:
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PCT-US95-17083-3
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                        ValGlnLeuLeuArgAsnTrpH1sGlnLeuH1sGlyLysLysGluAlaTyrAspThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC:1994
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
                                                                                                                                                                                                                                                                                   CONCURRENTLY HEREWITH
                                                                                                                                                                                              Sequence 9, Application PC/TUS9517083 GENERAL INFORMATION:
                                                                                                                                  1163 CTCAAGGACATTACT 1177
                                                                                                                        LeuLysAspileThr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 857 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-884-987-2_COPY_175_319 (1-145)_x PCT-US95-17083-3 (1-1104)
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APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                SECRETED HUMAN FAS ANTIGEN 16
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Indels:
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                                                                                                                                                                        : USSN 08/371,263
                                                                 NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
FILING DATE: CONCURRENTLY HERBAITH
Sequence 3, Application PC/TUS9517083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08444231
Patent No. 5652210
                                                                                                                                                                                                                                                                                                                                                                                  663.00
100.00%
100.00%
88.40%
                                                                                                                                                                                       23-DEC-1994
                                                                                                                                                                                                                                           LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity:
                                                                                                                                                                                            FILING DATE:
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SerLysTyrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
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                                                                                                                                                                   APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
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                                                    1059 ATTCAGACTATCATCCTCAAGGACATTACT 1088
                    136 IleGlnThrIleIleLeuLysAspIleThr 145
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                                                                                                  US-08-152-443A-18
: Sequence 18, Application US/08152443A
: Patent No. 5663070
: GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
                                                                                                                                                                                                                                                                                   3: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2
FELECOMMUNICATION INFORMATION
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243
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CORRESPONDENCE ADDRESS:
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STREET: 755 ...
CITY: Palo Alto
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Best Local Similarity:
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                     ADDRESSEE:
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US-08-152-443A-18
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TELEX: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
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                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 18-MAY-1995
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Mismatches;
Indels:
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152,443
FILING DATE: 15-NOV-1933
ATORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
RECISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-2000
TELECOMMUNICATION INFORMATION:
TELEFANS: (415) 813-5600
TELEFANS: (415) 494-0792
TELEFANS: (615) 494-0792
TELEFANS: 706141
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                 Eloppy disk
IBM PC compatible
:: MORRISON & FOER 755 Page Mill Road
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100.00%
88.40%
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243
                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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195..1136
                                Palo Alto
California
                                                                                                                                              OPERATING SYSTEM:
                                                                               94304-1018
                                                                                                                                                                                                             FILING DATE: 18
CLASSIFICATION:
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Best Local Similarity:
Query Match:
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LOCATION:
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                                                 STATE:
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TTIGIT 878		GluLys 135	; GENERAL INFORMATION: ; APPLICANT: Dean, Nicholas M. ; APPLICANT: Marcusson, Eric G. ; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling	; FILE REFERENCE: ISPH-0351 ; CURRENT APPLICATION NUMBER: US/09/290,640 ; CURRENT FILING DATE: 199-04-12 ; NUMBER OF SEQ ID NOS: 85 ; SOFTWARE: PatentIn Ver. 2.0	65 1480 A	; ORGANISM: Mus musculus ; FEATURE: ; NAME/KEY: CDS	; LOCATION: (50)(1033) ; PUBLICATION INFORMATION: ; JOURNAL: J. Immunol.	PAGES: 1274-1297 ; DATE: 1992-02-15 ; DATBASE ACCESSION NUMBER: M83649/Genbank ; DATABASE ENTRY DATE: 1994-04-18 US-09-290-640-65	nment Scores:	Pred. No.: 1.83e-31 Length: 1480 Score: 314.50 Matches: 69 Percent Similarity: 66.67% Conservative: 27 Best Local Similarity: 47.92% Mismatches: 43 Query Match: 41.93% Indels: 5 DB: 4 Gaps: 3	US-09-884-987-2_COPY_175_319 (1-145) x US-09-290-640-65 (1-1480)	Qy 2 TrpLeuCysLeuLeuLeuLeuLeuProlleProLeulleValTrpValLysArgLysGlu 20	Db 560 TGGTTGTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTT	OY 2.1 VALGATHEYSTHICTS ANGLE	484 Qy 41 LeuAsnProGluThrValAlalleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60	60 Db 668 TCCAGTCGTGAACCATACCAATGCCTCAAATCTTAGCTTGAGTAAATACTCCG	ATCACC 535 Qy 61 ThrilealaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80	595 Qy 81 ASnGluAlaLySILeASpGluIleLySASnASPASnValGlnASpThrAlaGluGlnLyS		GAA 655 Qy 101 ValGinLeuLeuArqAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
DD 819 ACTAAATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTT Qy 76 ArgLygasnGlyValasnGlualaLysIleaspGluIleLysAsnAspAsnValGL Dh 879 CGAAAGAATGGTCAAAAAAAAAGGACAAAAAAAAAAAAA	939 ACAGCAGAAAGTTCAACTGCTATTGGCATCAACTTCTTTATTCTTCTTCTTCTTTTTTTT	Oy 116 AlaryrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGl.	Oy 136 IleGlnThrIleIleLeuLysAspileThr 145 	RESULT 11 PCT-US95-17083-5 ; Sequence 5, Application PC/TUS9517083 ; GENERAL INFORMATION:	APPLICANT: TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN NUMBER OF SEQUENCES: 16	CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/17083 FILING DATE: CONCURRENTLY HEREWITH	CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION UNMBER: USSN 08/371,263 FILING DATE: 32-DEC-1904	ARACJ ARACJ 975 h cleic ESS:	; TOPOLOGY: linear PCT-US95-17083-5	Alignment Scores: 4.8e-63 Length: 975 Score: 554.50 Matches: 117 Percent Similarity: 80.69% Conservative: 0 Best Local Similarity: 7, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3,	S Gaps:	US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-5 (1-975)	1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeulleValTrpValLysArg	Oy . 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerPr	Db 484	41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyr	Db 485GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATAT Oy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLySGlyPheValArgLySAsnGl	'n	Oy 81 AsnGlualaLysIleAspGluIleLysAsnAspAsnVaiGlnAspThrAlaGluGlnLys	Db 596 AATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGAACA

PP1546

30-JAN-1998

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PRIOR APPLICATION DATA:
                                                        APPLICATION NUMBER:
                                                                          FILING DATE:
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121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
                                   908 ATCAAGGGTCTCAAAAAGCCGAATGTCGCAGAACCTTAGATAAATTTCAGGACATGGTC 967
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TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                          FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 149, Application US/09221017B
                                                                                                                                                                                     equence 15, Application PC/TUS9517083
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : MORRISON & FOERSTER
755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.000157
99.50
55.00%
55.00%
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                                                                                                                                                                                                                          APPLICANT: SECRET TITLE OF INVENTION: SECRET NUMBER OF SEQUENCES: 16 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT.
                                                                                                 HIIIII::
968 CAGAAGGACCTT 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                        141 LeuLysAspile 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM MEDIUM TYPE: Disket
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: (22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: ROSS, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lest Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
PCT-US95-17083-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                         Sequence 15,
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59 IleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsn 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AACGTGGATGAGGCGGATACGATCCTGGTCAATACCTGTTCGGTACGGGACAATGCCGAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 GlnLysVal---GlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 AspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGln 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 ------ValAlaIleAsnLeuSerAspValAspLeuSerLysTyr 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 GlyvalAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGlu 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- TTGGGCTGCATGGCCGAGCGCGTCAAG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 CTCTACATCGAGACCTATGGCTGCCAGATGAACGTAGCCGACAGTGAGGTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 LysHisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnProGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-884-987-2_COPY_175_319 (1-145) x US-09-221-017B-149 (1-478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: PORYPHYROMONAS GINGIVALIS FEATURE:
                                                                           PCT/AU98/01023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 TCCCGTCTCGTTATCGGGGTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GAGGAGTTGATCCGCGAA 48
                                                                                                                                                                                                            ELECOMMUNICATION INFORMATION
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                          NAME: Monroy, Gladys H
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1...478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.83%
24.60%
10.93%
                                                                                                                                                                                                                                                                                                                                                 478 base pairs
                                                                                                                                                                                                                                                                           TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                double
                                                                                                                                                                                                                                                                                                                                                                                                                     circular
                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: CIrcure
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
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1693 ACTIGC-----AAAGAAGAGTCGACTTCCAGACCAAGCCATCTTTGATAAC--- 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 LysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLysVal---Gln 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnPro 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 GluThrValAlalleAsnLeuSerAspValAspLeuSerLysTyrIleThrThrIleAla 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 GlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyValAsnGluAla 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-884-987-2_COPY_175_319 (1-145) x US-08-444-005-14 (1-2268)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 LeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAla 116 :::||||::: ||| |||
                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                              3: Fish & Richardson P.C.
225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REPERENCE/DOCKET NUMBER: 00383/026001
ELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                          Seed, Brian
Stanger, Ben 2.
Lee, Tae-Ho
Kim, Emily
FUNTION: CELL DEATH PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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Application US/08444005
                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
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29.79%
10.87%
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                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                        FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
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Best Local Similarity
                                                                                                                                                                                                              ADDRESSEE:
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                                                            APPLICANT
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Search completed: June 15, 2003, 22:59:24 Job time : 69 secs

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Sequence 998, App
Sequence 101, App
Sequence 1117, A
Sequence 1317, A
Sequence 1317, A
Sequence 99, Appl
Sequence 91, Appl
Sequence 28, Appl
Sequence 6140, App
Sequence 6140, Appl
Sequence 6140, Appl
Sequence 1140, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 138, Appl
Sequence 138, Appl
Sequence 138, Appl
Sequence 14730, Appl
Sequence 647, Appl
Sequence 14730, A
                       Sequence 8, Appli
Sequence 102, App
Sequence 17119, A
Sequence 2490, Ap
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Sequence 8513, Ap
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Sequence 3000,
Sequence 1, App
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145
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TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,713
CURRENT FILING DATE: 2001-09-12
PRIOR PAPLICATION NUMBER: US/09/180,100
PRIOR PLING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
PRIOR FILING DATE: 1997-05-01
SEQ. ID NO SEC. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-974-300-188
US-09-864-761-20550
US-09-864-761-3784
US-09-815-242-8513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-864-761-7040
US-09-974-300-3000
US-10-329-960-1
US-09-917-8008-1464
US-09-861-451A-29
                    US-09-963-2068-8

US-09-963-2068-8

US-09-9102-69-102

US-09-967-701-3156

US-09-945-531-998

US-09-918-995-1310-98

US-09-918-995-13045

US-09-918-995-13045

US-09-918-995-13045

US-09-918-995-1305

US-09-918-995-1395

US-09-918-995-1395

US-09-918-915-1310

US-09-911-536-8

US-09-911-536-8

US-09-911-536-8

US-09-911-536-8

US-09-911-536-8

US-09-911-536-8

US-09-911-536-8

US-09-911-536-8

US-09-911-536-8

US-09-911-314-13
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US-09-783-066-6
US-09-918-995-14730
US-09-742-096-4
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Matches:
Conservative:
Mismatches:
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Patent No. US20020044944A1
GENERAL INFORMATION:
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100.00%
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Percent Similarity:
Best Local Similarity:
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-Q-/cgn2_1/USPTO_spool/US09884987/runat_09062003_140302_13292/app_query.fasta_1.327,
-Q-/cgn2_1/USPTO_spool/US09884987/runat_09062003_140302_13292/app_query.fasta_1.327,
-DB-bublished_Applications_NA -QFMT=fastap -SGFFIX-P2n.rnpb -MINMATCH=0.1.
-LOOPCIL-0 -LOOPEXT=0 -UNITS-bits -START=1 -END--1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN=00 -THR_SCORE=pct -THR_MAX=100
-MAXIEN-200000000 -USER-GS9884987_GCGN -1.1.104_grunat_09062003_140302_13292
-NCPU=6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_INMEOUT=120 -WARM_INMEOUT=30 -THREADS=1 -SCAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Appl
Sequence 1, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Appli
                                                                                                                (without alignments)
1615.145 Million cell updates/sec
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1 GWLCLLLLPIPLIVWVRRKE......RANLCTLAEKIQTIILKDIT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                      protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-949-713-16
US-09-884-987-1
US-09-802-669-1
US-09-966-976A-7
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                                                                                                                                                                                                                                                                                                              1029858 segs, 724030393 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_NA:*
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7.0
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Maximum DB seq length: 2000000000
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US-09-884-987-2_COPY_175_319 (1-145) x US-09-949-713-16 (1-2534) US-09-884	1 1 1 1 1 1 1 1 1 1
LysGlu 20 AAGGAA 776 ACCACC 836 	GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu
ProThr 40 CCAACC 836 ATCACC 896 GGTCC 956 CGAAA 1016 Threw 120	ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
11eThr 60 ATCACC 896 GlyVal 80 GGTGTC 956 GlnLys 100 CAGAAA 1016	LeuasnProGluthrValalaIleasnLeuSeraspValaspLeuSerLysTyrIleThr
Glyval 80 GGTGTC 956 GlnLys 100 CAGAAA 1016	ThrilealaGlyValMetrhrLeuSerGlnValLySGlyPheValArgLySAsnGlyVal
GlnLys 100 CAGAAA 1016 ThrLeu 120	
ThrLeu 120	ValGinLeuLeuArgAsnTrpHisGinLeuHisGiyLysLysGluAlaTyrAspThrLeu
GIICAACIGCTICGIAAIICGCAICAACIICAIGGAAAGAAGAAGCGIAIGACATIG 1076 Db	1017 GITCAACTGCTLCGTAATTGGCATCAACTTCATGGAAAGAAGAAGAAGCGTATGACACATTG 1076
IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140 Oy	121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
Leulysaspilethr 145	141 LeuLysaspileThr 145.
SULT 2 -09-884-987-1 Sequence 1, Application US/09884987 Sequence 10. US20020102653A1 Setting	SULT 3 -09-802-669-1 Sequence 1, Application US/09802669 Patent. No. US20020004490A1 PAPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G.
: US/09/884,987 -06-21 3.0	APPLICANT: Wyatt, Jacqueline APPLICANT: Zhang, Hong TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REPRESENCE: ISPH-545 CIRBENT ADDITORING MIMBED: 18-00-0003 6-60
	THE STATE OF THE TOTAL OF THE TABLE TO THE TABLE TAB
	PRIOR APPLICATION NUMBER: US 09/290,640 PRIOR FILING DATE: 1999-04-12 NIMPER OF SEO ID NOS: 180
(1831)(1835) ; SOFT ; SOFT ; SEQ I ; SEQ I	PatentIn v
	LENGTH: 2551 TYPE: DNA PROPARTEM: Home canions
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(2352)(2357) ; PUBL polyA_site ; 500 ; VOL (2518)(2532) ; VOL	
2.79e-87 Length: 2534 DATABASE 750:00 Matches: 145 DATABASE 750:00:00:00:00:00:00:00:00:00:00:00:00:0	LISSUE: 15 PAGES: 10709-10715 DATE: 1992-05-25 DATABASE ACCESSION NUMBER: x63717/Genbank DATABASE ENTRY DATE: 1996-07-19

Ouery Match: 100.00% Indels: 0 DB: 9 Gaps: 0 US-09-884-987-2_COPY_175_319 (1-145) x US-09-966-976A-7 (1-8282) Oy 1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeulleValTrpValLysArgLysGlu 20 HILLHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Oy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40		101 ValginleuleuargasnTrpHisGinleuHisGiylysLysGiualaTyraspThrleu 	DD 4041 ATTARAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAAAATTCAGACTATCATC 3982 QY 141 LeuLysAspileThr 145	RESULT 5 US-09-963-206B-7/C Sequence 7, Application US/09963206B	GENERAL INFORMATION: APPLICANT: Ferrick, David A. APPLICANT: Swift, Susan E. APPLICANT: Swift, Susan E. APPLICANT: Swift, Susan E. APPLICANT: Fox, Bryan TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige TITLE OF INVENTION: Secretion and Switch Rearrangement TITLE OF INVENTION: WIMBER: US/09/963,206B CURRENT APPLICATION NUMBER: US/09/963,206B CURRENT FILING DATE: 1998-05-12 PRIOR APPLICATION NUMBER: US 09/076,624 NUMBER OF SEQ ID NOS: 19 SOFTWARE: Patentin version 3.1 SEQ ID NO 7 LEMENT REAL SASS		Alignment Scores: 1.61e-86 Length: 8282 Pred. No.: 750.00 Matches: 145 Score: 750.00 Matches: 145 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 10 Gaps: 0	US-09-884-987-2_COPY_175_319 (1-145) x US-09-963-206B-7 (1-8282)
Alignment Scores: 2.82e-87	GlyTrpLeuCysLeuLeuLeuLeuProlleProLeullevalTrpValLysArgLysGlu 	41 LeuasnProGluThrValAlaileAsnLeuSerAspValAspLeuSerLysTyrileThr 11	. 81 983 101	Db 1043 GTTCAACTGCTTCGTAATTGCAACTTCATGGAAGAAGAAGATGTTGTTGTTG 1102 Qy 121 IleLysAspLeuLysAspLeuCysThrLeuAlaGluLysIleGluThrIleIle 140 1103 ATTAAAGATCTCAAAAAAGCCAATCTTTGTTTTTTTTTT	LeuLysAspileThr 145 	RESULT 4 US-09-966-976A-7/C Sequence 7, Application US/09966976A Patent No. US20020168649A1 Sequence 7. Application US/09966976A Patent No. US20020168649A1 SERIERAL INFORMATION: APPLICANT: Ferrick, David A. APPLICANT: For, Bryan TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Syn TITLE OF INVENTION: Secretion and Switch Rearrangement FILE REFERENCE: A-66038-4/RMS/JJD/OLR CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION UNDER: US 09/076,624	PRIOR FILING DATE: 1998-05-12 NUMBER OF SEQ ID NOS: 19 SOFTWARE: PatentIn Version 3.1 SEQ ID NO.7 LENGTH: 8282 TYPE: DNA	ial sequence : synthetic 1.61e-86	Conservative: Mismatches:

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APPLICANT: Swift, Susan E.
APPLICANT: Swift, Susan E.
APPLICANT: Armstrong, Randall
APPLICANT: Armstrong, Randall
APPLICANT: Fox, Bryan
TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige
TITLE OF INVENTION: Secretion and Switch Rearrangement
FILE REFERENCE: A-66038-3/RMS/JJD/DLR
CURRENT APPLICATION NUMBER: US/09/963, 206B
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 1998-05-12
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                                            US-09-884-987-2_COPY_175_319 (1-145) x US-09-963-206B-8 (1-8345)
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Query Match:
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TITLE OF INVENTION: Methods and Compositions for Soreening for Modulators and Ige Syn
TITLE OF INVENTION: Secretion and Switch Rearrangement
TITLE OF INVENTION: Secretion and Switch Rearrangement
FILE REFERENCE: A-66038-4/RMS/JJD/DLR
FILE REFERENCE: A-66038-4/RMS/JJD/DLR
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 09/076,624
PRIOR FILING DATE: 198-05-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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APPLICANT: Swift, Susan E.
APPLICANT: Armstrong, Randall
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ThralaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu
                                                                          ACAGCAGAACAGAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAA
                                                                                                          AlaTyrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys
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Fublication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01.20
NUMBER OF SEQ ID NOS: 38054
SEQ ID NO 17119
LENGTH: 490.
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LOCATION: (1)...(490)
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OTHER INFORMATION: n
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Sequence 102, Application US/09802669
Fatent No. US20020004490A1
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Myatt, Jacqueline
APPLICANT: Myatt, Jacqueline
APPLICANT: Myatt, Jacqueline
APPLICANT: Myatt, US/09/802,669
TITLE OF INVENTON: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin. Ver. 2.0
SEQ ID NO 102
LENGTH: 836
                           515
                                                                                                                                                       ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
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 4281 TTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-09-802-669-102
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SEQ ID NO 998
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APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THI
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 20121.497
CURRENT PAPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastEEQ for Windows Version 4.0
SEQ ID NO 2490
LENGTH: 398
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.Matches:
.Conservative:
.Mismatches:
.Indels:
Gaps:
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Patent No. US20020132237A1
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601.00
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80.13%
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LOCATION: (1)...(398)
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; OTHER INFORMATION: n
US-09-867-701-2490
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Best Local Similarity:
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                                                                           -09-867-701-2490
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 136
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GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 AsnValGlnAspThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHis 111
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AND DIAGNOSIS OF OVARIAN CANCER
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                                                                                                                                                                                                                                                                                                                  Length:
                   FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ 1D NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
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566.00
99.12%
98.25%
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ORGANISM: Homo sapiens
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US-09-918-995-13045
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US-09-802-669-101
US-09-802-669-101
Sequence 101, Application US/09802669
Fatent No. US20020004490A1
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Myatt, Jacqueline
APPLICANT: Whatt, Jacqueline
APPLICANT: Application underse Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
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                                                  Matches:
Conservative:
Mismatches:
Indels:
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SEQ ID NO 101
LENGTH: 1840
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                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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: LOCATION: (95)
US-09-802-669-101
US-09-954-531-998
                         Alignment Scores
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Alignment Scores:

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                                                                                                               US-09-884-987-2_COPY_175_319 (1-145) x US-09-802-669-101 (1-1840)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13045, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION: ROWEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 1999-01-07-30
PRIOR FILING DATE: 1999-01-20
                            Conservative:
Mismatches:
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SOFTWARE: FastSEQ for Windows Version 3.0
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LOCATION: (1)...(489)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapiens
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Query Match:
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LysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIleLeu 141
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                                                                                                                                                                                      ## Sequence 15171, Application US/09918995

| Sequence 15171, Application US/09918995
| Publication No. US20030073623A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
| TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
| FILE REFERENCE: 20411-756
| CURRENT APPLICATION NUMBER: US/09/918,995
| CURRENT FILING DATE: 1999-01-20
| PRIOR FILING DATE: 1999-01-20
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Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity:
Query Match:
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LENGTH: 496
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BQ051037 1055 bp mRNA linear EST 29-MAR-2002
AGENCOURT_6954504 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5785846
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AA852070 HGBBT116
AK002590 Mus muscu
BI766250 603052708
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AV715411 AV715411
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AA745982 ob18912.s
AJ392468 AJ392468
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BF126149 601650407
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Eukaryota; Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1055)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AA293570 zt25h11.r
AA860068 HGBBT125
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Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-Q-Cgn2_1/CBPTO_spool/USO984987/runat_09062003_140300_13188/app_query.fasta_1.327
-Q-Cgn2_1/CBPTO_spool/USO9884987/runat_09062003_140300_13188/app_query.fasta_1.327
-QCGD_spool/USO98984987.runat_opun62 -TRANS-human40.cd1 -LIST-45
-UNITS-bits -START=1 -END-1 -NATRIX-bloum62 -TRANS-human40.cd1 -LIST-45
-DCCALIGN-200 -THR_SCORE-PLAKX-100 -TRR_MINO_0 -ALIGN-15 -MODE-LOCAL
-OGTFWT-009884987_CGGN_11_1525_GTUNAT_09062003_140300_13188 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY NEG_SCORES-0 -WAIT -DSPELOCK=100 -LONGLOG
-FGAPON-17 -YGAPOP-10 -YGAPEXT-0.5 -PGAPOP-6
-FGAPOP-10 -YGAPEXT-0.5 -DELEXT-7
                                                                                                   June 15, 2003, 21:50:09; Search time 1418 Seconds (Without alignments) 1656.097 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                  nucleic search, using frame_plus_p2n model
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Xgapop 10.0 , Xgapext
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TaE05016A

Tetraodon

ku06q01.1

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121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGlu 134
     AV651157.1 GI:9872171
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/tissue_type-"leiomyosarcoma"
/tis_host-"DH10B (phage-resistant)"
/note-"Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
a 221 c 215 g 267 t
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                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12873 row: j column: 23
High quality sequence stop: 689.
Location/Qualifiers
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Mismatches:
Indels:
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Matches:
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/db_xref="taxon:9606"
/clone="IMAGE:5785846"
               Ph.D.
Unpublished (1999)
Contact: Robert Strausberg, P
Emall: cgapbs-r@mall.nih.gov
Tissue Procurement: ATCE
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li;N., Du,J., Hu,M., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Chen,Z. and Han,Z.

Insight into hepatocelular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                                                                                                                                 Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
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Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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Mismatches:
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/db_xref="taxon:9606"
/clone="GLCCMD03"
/clone_lib="GLC"
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BI254532 776 bp mRNA linear EST 17-JUL-2001 602978522F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123477 5',
                                                                                                    ThralagluglnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu 115
                                                                                                                                                                                  116 AlatyrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135
                                                                                                                                                                                                                                                                134 AGTAAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 776)
NIH-MGC http://mgc.nci.nih.gov/.
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      SerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal
                                                                                    ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAsp
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Clone distribution: MGC clone distribution information can |
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1301 row: 1 column: 06
High quality sequence stop: 757.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapDs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
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Indels:
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Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_12"
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/seripts/gethtmi2.pl?tl=&t2=RC1-BN0039-060

Sudo-oll-a05&t3=2000-02-06&t4=1)

Seq primer: puc 18 forward
                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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1 (basel to 509)
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/note="Organ: breast_normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
                                                                                                  EST 05-JUN-2000
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55
                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                           roc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="BN0039"
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High quality sequence stop: 509.
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AUTHORS
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W05802 676 bp mRNA linear EST 23-APR-1996 za89505.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299745 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN ); mRNA sequence.
W05802 GI:1278534
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

[1] (Dases I to 676)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,The WashUr Merc Est Project

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                  Laboratories (Palo Alto,
                                                                                                                                                                                                                                      LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
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way, Box 8501, St. Louis,
                CA). Note: this is a NIH_MGC Library.
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140
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Mismatches:
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Matches:
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   constructed by
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Washington University School
4444 Forest Park Parkway, Box
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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644.50
97.24%
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Best Local Similarity:
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                                                                                 Alignment Scores:
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pbNR-Lib (clontech); Site_1:
/note="Organ: liver; Vector: pbNR-Lib (clontech); Site_1:
Sfil (gaccactaggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence:
5'-CACGGCCATANGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGGGCGGGCGCGCGAATG-4T(30)BN-3' (where B = A,
c, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb): 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nRNA linear EST 24-OCT-2000 CDNA clone IMAGE:3934273 5',
                                                                                                                                                                                                                                                                                                                                                           233
                                                                                                                                                                                                                                    80 lAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLy 100
                                                                                                                                                                                                                                                    sValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysLysGluAlaTyrAspThrLe 120
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1 (bases 1 to 809)

NIH-MGC http://mgc.ncl.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. CONSORTIUM (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM774 row: n coluum: 02
High quality sequence stop: 635.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF126149 809 bp m
601650407F1 NIH_MGC_76 Homo sapiens
mRNA sequence.
BF126149
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone-"IMAGE: 3934273"
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Euteleostomi;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases, 1 to 395)
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606.50
96.03%
93.65%
80.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stringency 81 c
                                                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                             1. .395
                                                                                                                                              sequence tags
               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aGluGlnLysValGlnLeuLeu-ArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAACAGAAAGTTCAACTGCTTCCGTAATTGGCATCAACTTCATGGAAAGAAGAAGGGGT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleG 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET.
High quality sequence stop: 307.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerProThrLeuasnProGluThrValAlaIleasnLeuSerAspValAspLeuSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLySGlyPheVal-ArgLy
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                                                                                                                                                                                                                                                                                                     9 others
                                                                                                         /clone="IMAGE:299745"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (amplcillin resistant)"
                                                                                                                                                                                                                                                                                                                                                    676
126
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Matches:
Conservative:
Mismatches:
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QV4-BT0407-020300-122-d09 BT0407 DE070451
BE070451.1 GI:8415097
                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACTATCATCCTCAAGGACATTACT 402
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                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                     127 c
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618.00
96.92%
96.92%
82.40%
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Best Local Similarity:
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/dev_gatge="Adult"
//dev_gatge="Adult"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=6t2-0V4-BT0407-020 300-122-d096t3=2000-03-026t4=1)
Seq primer: puc 18 forward High quality sequence start: 50 High quality sequence stop: 395.
Dias Neto'E., García Correa, R., Verjovski-Almelda, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,
Gencaration and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 31-DEC-1996
                                                                                                                                                                                                                       zo93g12.rl Stratagene ovarian cancer (#937219) Homo sapiens CDNA
clone IMAGE:594502 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR
(HUMAN); mRNA sequence.
                                              ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAla---TyrAspThr 119
                                                                        84 GIICAACIGCIICGIAAIIGGCAICAACIIITIAAAACACGGGAAAAGIAGIAIGACACA 25
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 263.
Location/Qualifiers
/clone_lib="Stratagene ovarian cancer (#937219)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-884-987-2_COPY_175_319 (1-145) x AA180032 (1-398)
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Mismatches:
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Matches:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:594502"
                                                                                                                                                                                                        398 bp
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AA180032.1 GI:1761298
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                       human.
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                                                                                                         120
              144
                                            101
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SOURCE
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AUTHORS
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AA180032
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HisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAla 47

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Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 460)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., Duduque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucabb,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor NDHOT HOMO saplens cDNA clone
to 9D:M67454 FASL RECEPTOR PRECURSOR (HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 08-AUG-1997
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                                                                                                                                                       182
                                                                                                                                                                                  127
                                                                                                                                                                                                                                                                                           302
                                                      67
87
                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1853 Std Error: 0.00 Seq primer: -28ml3 rev2 ET from Amersham
                                                   IleAsnLeuSerAspValAspLeuSerLysTyrIleThrThrIleAlaGlyValMetThr
                                                                                                                                                                                                                                                                                                                      MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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/db_xref="GDB:5934710"
                                                                                                                                                                                                                                                                                                                                                                                                                               460 bp
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/clone="IMAGE:714213"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          zt25h11.rl Soares ovary
IMAGE:714213 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA293570.1 GI:1941237
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AA293570
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122
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AUTHORS
TITLE .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA860068 305 bp mRNA linear EST 11-MAR-1998
HGBBT125 Human Glialblastoma Cell Homo sapiens cDNA, mRNA sequence.
AA860068
                                                                                                                                                                                                                                                                                                                                              61 GATGTTGACTTGAGTAAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTT 120
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                                                                                                                                                                                                                                 51
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                 AsnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSer
                                                                                                                                                                                                                                              52 AspValAspLeuSerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnVal
     pT7T3
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Jin, H.L., H.L., H.S.N., Tu.C., Yuan, J.G. and Qiang, B.Q.
DDRT-PCR of Human Glialblastoma Cell Line BT-325 cDNAs
  sites of a modified p
constructed by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human Glialblastoma Cell"
/cell_type="Glialblastoma Cell"
/cell_line="BT-325"
/lab_host="E.Coli DH5a"
                                                                                                                                                                                                     US-09-884-987-2_COPY_175_319 (1-145) x AA293570 (1-460)
                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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the Not I and Eco RI
(Pharmacia). Library
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                               M.Fatima Bonaldo.
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566.00
99.12%
98.25%
75.47%
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C
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Fax: 8610-5240529
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                                                                                                                                              Best Local Similarity:
                                             175
                                                                                                                                Percent Similarity:
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                                                                                       Alignment Scores:
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                                            BASE COUNT.
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VERSION
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SOURCE
ORGANISM
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TITLE
JOURNAL
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AGENCOURT_6652776 NIH_MGC_118 Homo saplens cDNa clone IMAGE:5755724 BM922638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1152)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAsp 95
was isolated from human glialblastoma cell line BT325. Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell. Differentially expressed PCR products were cloned and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu
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96
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Contact: Robert Strausberg, Ph.D.
Email: cgabbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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/clone_lib="NIH_MGC_118"
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/db_xref="taxon:9606"
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High quality sequence stop: 628
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Best Local Similarity:
Query Match:
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210
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 696)

Xu,X., Gu,J., Liu,F.; Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
Homo saplens.cDNA DCB clones
            /note="Vector: pcMv-SpORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range lil.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NHLMGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 ThralaGlu-GlnLysValGlnLeuLeuArgAsnTrp-HisGlnLeuHisGlyLys---L 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGCAGAAACAGAAAGTTCCACTGCTTTCCAATTGGGCATCAACTTCATGGGAAAGGAA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysGluAlaTyrAspThrLeu-IleLysAspLeuLysLysAla---AsnLeuCysThrLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAsp 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
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AV715411 DCB Homo sapiens cDNA clone DCBAUC01 5',
AV715411.1 GI:10796928
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Mismatches:
Indels:
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Matches:
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/lab_host-"DH10B"
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492.00
88.37%
84.50%
65.60%
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Best Local Similarity:
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AL542093 ALT_FL002_PL1 Homo sapiens cDNA clone CS0DE009xI06 5 prime AL542093 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE009xI06 5 prime AL542093
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Uni,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                   /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
141 c 156 g 189 t
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BP 191 91006 EVRY cedex - France
Emall: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Mismatches:
Indels:
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Matches:
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzgehgc.sh.cn
This clone is available at CHGC in
Location/Qualiflers
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/db_xref="taxon:9606"
/clone="CSODE009Y106"
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/clone="DCBAUC01"
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/dev_stage="mature"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualiflers
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426.00
98.82%
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Best Local Similarity:
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          /note="Organ: placenta; Vector: pcMvSpORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSpORT 6 vector. Library was constructed by Life Technologies. Contact: From plang Lilang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville division of Invitrogen 9800 Medical Center Drive Rockville filang@liletech.com.URL:
filang@liletech.com.URL:
210 c 233 g 218 t 1 others
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HGBBT116 Human Glialblastoma Cell Homo sapiens CDNA, mRNA sequence.
AA852070
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/colnc_lib="Human Glialblastoma Cell"
/cell_lipe="Glialblastoma Cell"
/cell_line="BT-325"
/lab_host="E.coli DH5a"
/note="Organ: Brain; Vector: PCRII, Invitrogen; Total RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Boqin Qlang
Mational Laboratory of Medical Molecular Biology, CAMS & PUMC
Mational Laboratory of Medical sciences, Peking Union Medical College
Chinese Academy of Medical Sciences
S Dong Dan San Tiao, Beljing 100005, P.R. China
Tel: (010)65296411
Fax: 8610-5240529
                                                                                                                                                                                                                                                                                                                                                                                                                                                   705 GGGTGGCTTTGTCTTCTTTTGCCAATTCCACTAATTGTTTGGGTGAAGGAAAGGAA 764
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Jin,H.L., Hu,S.N., Tu,C., Yuan,J.G. and Qiang,B.Q.
DDRT-PCR of Human Glialblastoma Cell Line BT-325 cDNAs
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
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Mismatches:
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Matches:
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/lab_host-"DH10B
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375.00
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50.00%
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Best Local Similarity:
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Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610012D23:tumor necrosis factor receptor superfamily, member 6, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 AGTAAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 196
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
was isolated from human glialblastoma cell line BT325. Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell. Differentially expressed PCR products were cloned and sequenced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mismatches:
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Matches:
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AK002590.1 GI:12832683
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Best Local Similarity:
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/tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .1437
                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="mGD:MGI:95484"
/translation="MLWIMAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVRETDKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL
CDEEHGLEVETNCTLTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRKOSPRNRLWLLTILVLLIPLVFIYRKYRKRKCWKRRODDPESRTSSRETIPNNASN
LSLSKYIPRIAEDWTIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ValGInLeuLeuArgAsnTrpHisGInLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 AGAATTGCTGAAGACATGACAATCCAGGAAGCTAAAAAATTTGCTCGAGAAATAACATC
                                                                                                                                                                                                                                                                                              tumor necrosis factor receptor superfamily, member 6"
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/gene="Tnfrsf6"
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/gene="Tnfrsf6"
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